GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:18:45 ; Search time 36 Seconds
(without alignments)
142.663 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1491	100.0	300	10	US-09-896-096A-1	Sequence 1, Appli
2	1491	100.0	300	10	US-09-894-924-1	Sequence 1, Appli
3	1491	100.0	300	10	US-09-935-727-2	Sequence 2, Appli
4	1476.5	99.0	299	10	US-09-877-156-17	Sequence 17, Appl
5	1469	98.5	300	10	US-09-840-795-2	Sequence 2, Appli
6	1034	69.3	211	10	US-09-877-156-20	Sequence 20, Appl
7	841	56.4	153	10	US-09-877-156-2	Sequence 2, Appli
8	671	45.0	170	10	US-09-935-727-4	Sequence 4, Appli
9	461	30.9	326	10	US-09-062-113-71	Sequence 71, Appl
10	442.5	29.7	401	10	US-09-062-113-62	Sequence 62, Appl
11	440.5	29.5	272	10	US-09-062-113-75	Sequence 75, Appl
12	440.5	29.5	293	10	US-09-896-096A-18	Sequence 18, Appl
13	440.5	29.5	293	10	US-09-894-924-18	Sequence 18, Appl
14	440.5	29.5	321	10	US-09-062-113-80	Sequence 80, Appl
15	440.5	29.5	327	10	US-09-062-113-72	Sequence 72, Appl
16	440.5	29.5	351	10	US-09-062-113-74	Sequence 74, Appl
17	440.5	29.5	362	10	US-09-062-113-11	Sequence 11, Appl
18	440.5	29.5	380	10	US-09-062-113-4	Sequence 4, Appli
19	440.5	29.5	391	10	US-09-062-113-106	Sequence 106, App
20	440.5	29.5	393	10	US-09-062-113-79	Sequence 79, Appl
21	440.5	29.5	399	10	US-09-062-113-73	Sequence 73, Appl
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26	440.5	29.5	401	12	US-10-039-785-5	Sequence 5, Appli
27	440.5	29.5	401	12	US-10-066-209-1	Sequence 1, Appli
28	440.5	29.5	401	12	US-10-164-592-2	Sequence 2, Appli
29	433.5	29.1	401	10	US-09-062-113-63	Sequence 63, Appl
30	433	29.0	187	10	US-09-062-113-81	Sequence 81, Appl
31	433	29.0	187	10	US-09-840-795-11	Sequence 11, Appl
32	433	29.0	197	10	US-09-062-113-76	Sequence 76, Appl
33	432	29.0	394	10	US-09-062-113-9	Sequence 9, Appli
34	407	27.3	147	9	US-09-756-854-20	Sequence 20, Appl
35	407	27.3	147	9	US-10-041-574-20	Sequence 20, Appl
36	356.5	23.9	360	10	US-09-062-113-67	Sequence 67, Appl
37	342.5	23.0	450	10	US-09-768-779A-3	Sequence 3, Appli
38	342.5	23.0	461	10	US-09-826-212-4	Sequence 4, Appli
39	342.5	23.0	461	10	US-09-896-096A-17	Sequence 17, Appl
40	342.5	23.0	461	10	US-09-894-924-17	Sequence 17, Appl
41	342.5	23.0	461	10	US-09-840-707A-17	Sequence 17, Appl
42	342.5	23.0	461	10	US-09-935-727-6	Sequence 6, Appli
43	340.5	22.8	461	10	US-09-800-909-2	Sequence 2, Appli
44	340.5	22.8	461	10	US-09-758-124-2	Sequence 2, Appli
45	340.5	22.8	461	10	US-09-800-908-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-896-096A-1
; Sequence 1, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/896,096A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 1
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-096A-1

Query Match 100.0%; Score 1491; DB 10; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.8e-107;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
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Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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RESULT 2
US-09-894-924-1
; Sequence 1, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/894,924
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 1
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-894-924-1

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Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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RESULT 3
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; Sequence 2, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-935-727-2

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RESULT 4
US-09-877-156-17
; Sequence 17, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
;  APPLICANT: Catherine Tribouley
;  TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
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;  FILE REFERENCE: 1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/877,156
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/286,529
;  PRIOR FILING DATE: 1998-04-05
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-877-156-17

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  Matches  270;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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Qy     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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RESULT 5
US-09-840-795-2
; Sequence 2, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Erin E.
;  APPLICANT:  Mattson, Jeanine D.
;  APPLICANT:  Bates, Elizabeth Esther Mary
;  APPLICANT:  Gorman, Daniel M.
;  APPLICANT:  Lebecque, Serge J.E.
;  TITLE OF INVENTION: Mammalian Genes; Related Reagents
;  FILE REFERENCE: SF0818K
;  CURRENT APPLICATION NUMBER: US/09/840,795
;  CURRENT FILING DATE:  2001-04-23
;  PRIOR APPLICATION NUMBER: 09/351,777
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: primate
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (79)
;   OTHER INFORMATION: Xaa at residue 79 is undetermined.
US-09-840-795-2

  Query Match             98.5%;  Score 1469;  DB 10;  Length 300;
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  Matches  268;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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Db     90 XCYVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy    121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
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Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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Db    270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 6
US-09-877-156-20
; Sequence 20, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
;  APPLICANT: Catherine Tribouley
;  TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE: 1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/877,156
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/286,529
;  PRIOR FILING DATE: 1998-04-05
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-877-156-20

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Qy    181 E 181
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Db    210 E 210


RESULT 7
US-09-877-156-2
; Sequence 2, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
;  APPLICANT: Catherine Tribouley
;  TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE: 1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/877,156
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/286,529
;  PRIOR FILING DATE: 1998-04-05
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 2
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: human
US-09-877-156-2

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Db       1 LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTP 60

Qy     116 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 120

Qy     176 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 208
           ||||||||||||||||||||||||||||||||
Db     121 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 153


RESULT 8
US-09-935-727-4
; Sequence 4, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-935-727-4

  Query Match             45.0%;  Score 671;  DB 10;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-44;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPG 113
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Db      90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPG 142


RESULT 9
US-09-062-113-71
; Sequence 71, Application US/09062113
; Patent No. US20020051969A1
;  GENERAL INFORMATION:
;    APPLICANT:  GOTO, Masaaki
;    APPLICANT:  TSUDA, Eisuke
;    APPLICANT:  MOCHIZUKI, Shin'ichi
;    APPLICANT:  YANO, Kazuki
;    APPLICANT:  KOBAYASHI, Fumie
;    APPLICANT:  SHIMA, No. US20020051969A1uyuki
;    APPLICANT:  YASUDA, Hisataka
;    APPLICANT:  NAKAGAWA, No. US20020051969A1uaki
;    APPLICANT:  MORINAGA, Tomonori
;    APPLICANT:  UEDA, Masatsugu
;    APPLICANT:  HIGASHIO, Kanji
;    TITLE OF INVENTION:  No. US20020051969A1el Proteins and Methods for Producing
;    TITLE OF INVENTION:  the Proteins
;    NUMBER OF SEQUENCES:  108
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/062,113
;      FILING DATE:  17-APR-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 54977/1995
;      FILING DATE:  20-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 207508/1995
;      FILING DATE:  21-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP96/00374
;      FILING DATE:  20-FEB-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/915,004
;      FILING DATE:  20-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MOORE, Ronda P.
;      REGISTRATION NUMBER:  44,244
;      REFERENCE/DOCKET NUMBER:  FJN-060DV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  326 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  -21..0
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..305
;      OTHER INFORMATION:  /note= "OCIF-DDD1"
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US-09-062-113-71

Query Match 30.9%; Score 461; DB 10; Length 326;
Best Local Similarity 33.1%; Pred. No. 2.8e-28;
Matches 94; Conservative 57; Mismatches 101; Indels 32; Gaps 7;

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Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||  :|:| :|||||:::: |     | | |||  :|| |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPG--AEEC 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  |   : |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDIDLC 202

Qy     183 ERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRR-----RLTELL- 236
           | :|   :   ::: ::|: |:::|       | : |   ::  ::       :: :||
Db     203 ENSVQRHIGHANLTFEQLRSLMESL-------PGKKVGAEDIEKTIKACKPSDQILKLLS 255

Qy     237 ------GAQDGALLVRLLQALRVARMPGLERSVRE------RFL 268
                 | ||   |  |: ||: ::     ::| :      |||
Db     256 LWRIKNGDQD--TLKGLMHALKHSKTYHFPKTVTQSLKKTIRFL 297
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RESULT 10
US-09-062-113-62
; Sequence 62, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; TITLE OF INVENTION: the Proteins
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibeault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,113
; FILING DATE: 17-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 54977/1995
; FILING DATE: 20-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207508/1995
; FILING DATE: 21-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00374
; FILING DATE: 20-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,004
; FILING DATE: 20-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MOORE, Ronda P.
; REGISTRATION NUMBER: 44,244
; REFERENCE/DOCKET NUMBER: FJN-060DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: -21..0
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..380
; OTHER INFORMATION: /note= "OCIF-C19S"
US-09-062-113-62

Query Match 29.7%; Score 442.5; DB 10; Length 401;
Best Local Similarity 41.2%; Pred. No. 9.1e-27;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

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Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||  :|:| :|||||:::: |     | | |||  :|| |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKSGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209
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RESULT 11
US-09-062-113-75
; Sequence 75, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; TITLE OF INVENTION: the Proteins
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibeault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/062,113
;       FILING DATE:  17-APR-1998
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 54977/1995
;       FILING DATE:  20-FEB-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 207508/1995
;       FILING DATE:  21-JUL-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP96/00374
;       FILING DATE:  20-FEB-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/915,004
;       FILING DATE:  20-FEB-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MOORE, Ronda P.
;       REGISTRATION NUMBER:  44,244
;       REFERENCE/DOCKET NUMBER:  FJN-060DV
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 248-7000
;       TELEFAX:  (617) 248-7100
;   INFORMATION FOR SEQ ID NO:  75:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  272 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  Peptide
;       LOCATION:  -21..0
;     FEATURE:
;       NAME/KEY:  Protein
;       LOCATION:  1..251
;       OTHER INFORMATION:  /note= "OCIF-CDD2"
US-09-062-113-75

  Query Match             29.5%;  Score 440.5;  DB 10;  Length 272;
  Best Local Similarity   41.2%;  Pred. No. 8.5e-27;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209


RESULT 12
US-09-896-096A-18
; Sequence 18, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/896,096A
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 18
;   LENGTH: 293
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-896-096A-18

  Query Match             29.5%;  Score 440.5;  DB 10;  Length 293;
  Best Local Similarity   41.2%;  Pred. No. 9.2e-27;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209


RESULT 13
US-09-894-924-18
; Sequence 18, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/894,924
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 18
;   LENGTH: 293
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-09-894-924-18

Query Match 29.5%; Score 440.5; DB 10; Length 293;
Best Local Similarity 41.2%; Pred. No. 9.2e-27;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

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Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209
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RESULT 14
US-09-062-113-80
; Sequence 80, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; TITLE OF INVENTION: the Proteins
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibeault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,113
; FILING DATE: 17-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 54977/1995
; FILING DATE: 20-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207508/1995
; FILING DATE: 21-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00374
; FILING DATE: 20-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,004
; FILING DATE: 20-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MOORE, Ronda P.
; REGISTRATION NUMBER: 44,244
; REFERENCE/DOCKET NUMBER: FJN-060DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: -21..0
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..300
; OTHER INFORMATION: /note= "OCIF-CSph"
US-09-062-113-80

Query Match 29.5%; Score 440.5; DB 10; Length 321;
Best Local Similarity 41.2%; Pred. No. 1e-26;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

```
Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
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Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
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Db     203 EEAFFRF 209
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RESULT 15
US-09-062-113-72
; Sequence 72, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; TITLE OF INVENTION: the Proteins
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibeault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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;      APPLICATION NUMBER:  US/09/062,113
;      FILING DATE:  17-APR-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 54977/1995
;      FILING DATE:  20-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 207508/1995
;      FILING DATE:  21-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP96/00374
;      FILING DATE:  20-FEB-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/915,004
;      FILING DATE:  20-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MOORE, Ronda P.
;      REGISTRATION NUMBER:  44,244
;      REFERENCE/DOCKET NUMBER:  FJN-060DV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  72:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  327 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  -21..0
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..306
;      OTHER INFORMATION:  /note= "OCIF-DDD2"
US-09-062-113-72

  Query Match             29.5%;  Score 440.5;  DB 10;  Length 327;
  Best Local Similarity   41.2%;  Pred. No. 1e-26;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
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Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
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Qy     183 ERAVIDF 189
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Db     203 EEAFFRF 209


Search completed: January  6, 2003, 11:27:02
Job time : 37 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:31 ; Search time 61 Seconds
(without alignments)
591.982 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1491	100.0	271	20	AAY42184	Human mFLINT #1 pr
2	1491	100.0	271	21	AAB19334	A mature human FAS
3	1491	100.0	271	21	AAB19705	Human FAS ligand i
4	1491	100.0	271	21	AAY97247	M68 TNF receptor r
5	1491	100.0	271	21	AAY96598	Human mature FLINT
6	1491	100.0	271	22	AAE03567	Human mature fas l
7	1491	100.0	271	22	AAB68044	Amino acid sequenc
8	1491	100.0	271	22	AAB68047	Amino acid sequenc
9	1491	100.0	271	22	AAB74465	Human FLINT mature
10	1491	100.0	271	23	AAE14578	Human mature FLINT
11	1491	100.0	300	19	AAW66102	Amino acid sequenc
12	1491	100.0	300	19	AAW63622	Human tumour necro
13	1491	100.0	300	20	AAY03099	Human lung TNF-rec
14	1491	100.0	300	20	AAY42182	Human FLINT #1 pro
15	1491	100.0	300	20	AAY17479	Mammalian tumour n
16	1491	100.0	300	20	AAY06817	Human DcR3 polypep
17	1491	100.0	300	20	AAW97749	Human tumour necro
18	1491	100.0	300	20	AAW95082	Orphan receptor (H
19	1491	100.0	300	21	AAB19335	A full length huma
20	1491	100.0	300	21	AAB28559	Human soluble TNF
21	1491	100.0	300	21	AAB24057	Human PRO212 prote
22	1491	100.0	300	21	AAB33416	Human PRO212 prote
23	1491	100.0	300	21	AAB03621	Human Fas ligand i
24	1491	100.0	300	21	AAY97246	M68 TNF receptor r
25	1491	100.0	300	21	AAY90357	Human tumour necro
26	1491	100.0	300	21	AAB24395	Human PRO212 prote
27	1491	100.0	300	21	AAY96596	Human FLINT. Homo
28	1491	100.0	300	22	AAE03568	Human native fas l
29	1491	100.0	300	22	AAB74466	Human FLINT native
30	1491	100.0	300	22	AAB71754	Human NTR3. Homo
31	1491	100.0	300	22	AAB48161	Human PRO212 polyp
32	1491	100.0	300	22	AAB50903	Human PRO212 prote
33	1491	100.0	300	23	AAE14579	Human native FLINT
34	1491	100.0	300	23	AAE20848	Human tumour necro
35	1491	100.0	341	22	AAG73740	Human colon cancer
36	1487	99.7	271	21	AAB19709	Protease-resistant
37	1487	99.7	271	22	AAE03571	Human mature fas l
38	1487	99.7	271	22	AAB74467	Human FLINT mature
39	1487	99.7	271	23	AAE14581	Human protease-res
40	1486	99.7	271	22	AAE03584	Human mature fas l
41	1486	99.7	271	23	AAE14582	Human protease-res
42	1485	99.6	271	21	AAY96599	Human mature FLINT
43	1485	99.6	271	23	AAE14583	Human protease-res
44	1485	99.6	271	23	AAE14584	Human protease-res
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ALIGNMENTS

RESULT 1
AAY42184
ID AAY42184 standard; Protein; 271 AA.
XX
AC AAY42184;
XX
DT 17-DEC-1999 (first entry)
XX
DE Human mFLINT #1 protein sequence.
XX
KW Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancytopenic condition;
KW myocardial ischaemia.
XX
OS Homo sapiens.
XX
PN WO9950413-A2.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US06797.
XX
PR 30-MAR-1998; 98US-0079856.
PR 20-MAY-1998; 98US-0086074.
PR 09-SEP-1998; 98US-0099643.
PR 17-DEC-1998; 98US-0112577.
PR 18-DEC-1998; 98US-0112703.
PR 18-DEC-1998; 98US-0112933.
PR 22-DEC-1998; 98US-0113407.
XX

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PA   (ELIL ) LILLY & CO ELI.
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PI   Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
PI   Hui KY, Kharitonenkov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
PI   Song HY, Wang J, Wu X, Zuckerman SH;
XX
DR   WPI; 1999-591319/50.
DR   N-PSDB; AAZ25377.
XX
PT   Use of mature FLINT for treating acute liver failure, inflammation,
PT   cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
PT   and proinflammatory activity
XX
PS   Claim 31; Fig 3; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   represents human mFLINT.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 20;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
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Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
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Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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Db     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 2
AAB19334
ID   AAB19334 standard; Protein; 271 AA.
XX
AC   AAB19334;
XX
DT   19-FEB-2001  (first entry)
XX
DE   A mature human FAS Ligand Inhibitory Protein (FLINT).
XX
KW   Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW   tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW   acute respiratory distress syndrome; ulcerative colitis;
KW   chronic obstructive pulmonary disease; Crohn's disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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PN   WO200058465-A2.
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PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06417.
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PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140077.
PR   21-JUN-1999;   99US-0140156.
PR   20-OCT-1999;   99US-0160566.
PR   18-FEB-2000; 2000US-0183398.
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PA   (ELIL ) LILLY & CO ELI.
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PI   Becker GW,  Cohen FJ,  Gonzalez-dewhitt PA,  Hale JE,  Micanovic R;
PI   Newton CM,  Noblitt TW,  Rathmachalam R,  Tschang SR,  Witcher DR;
PI   Wroblewski VJ;
XX
DR   WPI; 2000-656167/63.
DR   N-PSDB; AAA75999.
XX
PT   FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT   apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT   chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT   disease  -
XX
PS   Claim 1; Page 112-113; 114pp; English.
XX
CC   The present sequence represents a mature human FAS Ligand Inhibitory
CC   Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC   proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC   FLINT protein is modified to produce analogues, which have greater
CC   potency, longer in vivo half-lives, decreased aggregation, decreased
CC   absorption onto surfaces, increased solubility and improved ease of
CC   formulation. The FLINT analogue is useful for treating a patient
CC   suffering from disease or condition relating to abnormal apoptosis such
CC   as acute lung injury, acute respiratory distress syndrome, pulmonary
CC   fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC   Crohn's disease.
XX
SQ   Sequence   271 AA;

  Query Match            100.0%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity  100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
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Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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Db     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 3
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ID   AAB19705 standard; Protein; 271 AA.
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AC   AAB19705;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Human FAS ligand inhibitor protein FLINT.
XX
KW   FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW   acute lung injury; acute respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   ulcerative colitis; therapy; organ transplantation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                        Claims 10, 11, 13 and 14"
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FT                        occurring amino acid, preferably Tyr as
FT                        given in Claim 9"
FT   Misc-difference 218
FT                   /note= "optionally replaced by any naturally
FT                        occurring amino acid, preferably Gln, Glu,
FT                        Ala, Gly, Ser, Val, Tyr or Asn as given in
FT                        Claims, 9, 10, 11, 12, especially Gln as
FT                        given in Claims 13, 14, 15, 35 and 36"
FT   Misc-difference 219
```

```
FT                   /note= "optionally replaced by any naturally
FT                         occurring amino acid"
FT   Misc-difference 220
FT                   /note= "optionally replaced by any naturally
FT                         occurring amino acid"
FT   Misc-difference 221
FT                   /note= "optionally replaced by any naturally
FT                         occurring amino acid"
FT   Misc-difference 222
FT                   /note= "optionally replaced by any naturally
FT                         occurring amino acid"
XX
PN   WO200058466-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06418.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140073.
PR   04-AUG-1999;   99US-0147071.
PR   20-OCT-1999;   99US-0160524.
PR   21-OCT-1999;   99US-0160669.
PR   20-DEC-1999;   99US-0172744.
PR   26-JAN-2000; 2000US-0178184.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Rathnachalam R,  Witcher DR;
XX
DR   WPI; 2000-664925/64.
DR   N-PSDB; AAA88730.
XX
PT   Novel protease resistant FAS ligand inhibitory protein analogues
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases  -
XX
PS   Claim 1; Page 94-95; 100pp; English.
XX
CC   The present sequence is that of human FAS ligand inhibitory protein
CC   FLINT mature protein.  FLINT is a tumour necrosis factor receptor
CC   homologue that binds FAS ligand, preventing its interaction with
CC   FAS.  This interaction is implicated in runaway apoptosis and
CC   inflammatory disease.  FLINT also binds to LIGHT, a membrane-bound
CC   ligand, which may play a role in immune modulation and apoptosis.
CC   The invention relates to novel FLINT analogues (see also AAB19706-09)
CC   that are resistant to proteolysis by trypsin-like proteases between
CC   positions 218 and 219 of the FLINT mature protein sequence.  The
CC   analogues have amino acid substitutions in the region comprising
CC   amino acids 214-222, and may contain additional substitutions at
CC   residues 34, 36, 132, 194 and/or 196.  Nucleic acids, vectors and
CC   transformed host cells for recombinant production of the analogues
CC   are claimed.  FLINT cDNA (see AAA88730) is used as a template for
CC   introducing the required point mutations.  The protease resistant
CC   FLINT analogues are used to prevent or treat acute lung injury,
CC   acute respiratory stress syndrome, ulcerative colitis, chronic
CC   obstructive pulmonary disease, pulmonary fibrosis, to inhibit T
CC   lymphocyte activation, and to facilitate organ preservation for
CC   transplantation (claimed).
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy    121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy    181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          |||||||||||||||||||||||||||||||
Db    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 4
AAY97247
ID   AAY97247 standard; Protein; 271 AA.
XX
AC   AAY97247;
XX
DT   19-DEC-2000  (first entry)
XX
DE   M68 TNF receptor related protein (mature protein).
XX
KW   M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
KW   receptor; immune response; cell differentiation; ligand; cancer;
KW   bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
KW   Grave's disease; idiopathic myxodema; autoimmune diabetes;
KW   thrombotic thrombocytopenic purpura; multiple sclerosis;
KW   liver diseases; autoimmune gastritis; ulcerative colitis;
KW   glomerulonephritis; pulmonary fibrosis; heart failure;
KW   atherosclerosis; aplastic anaemia; myelodisplastic syndromes;
KW   osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
KW   myocardial infarction; human.
XX
OS   Homo sapiens.
XX
PN   WO200046247-A1.
XX
PD   10-AUG-2000.
XX
PF   04-FEB-2000; 2000WO-US03037.
XX
PR   05-FEB-1999;   99US-0118902.
PR   20-DEC-1999;   99US-0172754.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Bai C;
XX
DR   WPI; 2000-506066/45.
XX
PT   Isolated human M68 nucleic acids and proteins which are part of the
PT   tumor necrosis factor receptor (TNFR) family, useful for identifying
PT   modulators that may be used to treat various diseases e.g. cancer,
PT   osteoporosis, Alzheimer's disease
XX
PS   Claim 1; Page 76; 80pp; English.
XX
CC   The M68 protein is a member of a family of proteins which have
CC   roles in immune responses, cell death, cell proliferation and
CC   stimulation of cell differentiation. M68 lacks a transmembrane domain
CC   and is a secreted factor suggesting that it functions as a natural
CC   inhibitor for its ligand. The altered expression pattern of M68 in a
CC   multitude of tissues suggests that M68 may play a role in cancer by
CC   binding to its ligand and blocking apoptotic cell death induced by
CC   such a ligand. This anti-apoptopic role of M68 suggests that
CC   modulators of M68 will be useful in treatment of apoptosis-related
CC   diseases such as various forms of cancer and various bone disorders.
CC   M68 nucleic acids and proteins are therefore useful for treating
CC   conditions involving atypical apoptosis and for identifying
CC   modulators of M68. Modulators of M68 are useful for treatment of
CC   cancer and other diseases associated with abnormal levels of
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```
CC   apoptosis including systemic lupus erythematosus, Hashimoto's
CC   thyroiditis, Grave's disease, idiopathic myxodema, autoimmune
CC   diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
CC   liver diseases, autoimmune gastritis, ulcerative colitis,
CC   glomerulonephritis, pulmonary fibrosis, heart failure,
CC   atherosclerosis, aplastic anaemia, myelodisplastic syndromes,
CC   osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
CC   myocardial infarction.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          |||||||||||||||||||||||||||||||
Db     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 5
AAY96598
ID   AAY96598 standard; Protein; 271 AA.
XX
AC   AAY96598;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human mature FLINT.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   N-PSDB; AAA51077.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 8; Fig 3; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          |||||||||||||||||||||||||||||||
Db     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 6
AAE03567
ID   AAE03567 standard; Protein; 271 AA.
XX
AC   AAE03567;
XX
DT   04-AUG-2001  (first entry)
XX
DE   Human mature fas ligand inhibitory protein (FLINT).
XX
KW   Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
KW   TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KW   acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KW   chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
KW   rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
KW   fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KW   chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KW   vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KW   insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KW   Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KW   Down's syndrome; multiple sclerosis; cytostatic; nootropic;
KW   neuroprotective; vasotropic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   144
FT                   /note= "N-linked glycosylation site"
```

```
FT   Modified-site   174
FT                   /note= "O-linked glycosylation site"
FT   Modified-site   216
FT                   /note= "O-linked glycosylation site"
FT   Cleavage-site   218..219
FT                   /note= "Proteolytic cleavage"
XX
PN   WO200142463-A1.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US30166.
XX
PR   07-DEC-1999;   99US-0169367.
PR   07-DEC-1999;   99US-0169381.
PR   07-DEC-1999;   99US-0169412.
PR   23-MAR-2000; 2000US-0191430.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Lu J,  Witcher DR;
XX
DR   WPI; 2001-381684/40.
DR   N-PSDB; AAD07380.
XX
PT   New FLINT polypeptide for treating and/or preventing acute lung injury,
PT   acute respiratory distress syndrome, ulcerative colitis, and
PT   graft-versus-host disease, comprises O-linked or N-linked
PT   oligosaccharides -
XX
PS   Example 1; Page 52-53; 60pp; English.
XX
CC   The present sequence is human mature fas ligand inhibitory protein
CC   (FLINT). FLINT, a homologue of tumour necrosis factor receptor
CC   protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC   interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC   oligosaccharides is useful for preventing or treating acute lung injury
CC   (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC   chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC   to facilitate organ preservation for transplantation and to inhibit T
CC   lymphocyte activation. FLINT is useful for treating and/or preventing
CC   diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC   fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC   (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC   host disease, cutaneous inflammation, vascular leak syndrome,
CC   Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC   diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC   Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC   psoriasis, Down's syndrome, and multiple sclerosis.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          ||||||||||||||||||||||||||||||
Db     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 7
AAB68044
ID   AAB68044 standard; Protein; 271 AA.
XX
AC   AAB68044;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Amino acid sequence of a human mature FLINT polypeptide.
XX
KW   FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW   Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS   Homo sapiens.
XX
PN   WO200118055-A1.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20807.
XX
PR   10-SEP-1999;   99US-0153339.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-273382/28.
XX
PT   Compositions comprising a divalent metal cation and a FAS Ligand
PT   Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT   FLINT and for treating diseases involving FasL/Fas and/or
PT   LIGHT/LT-beta-R receptor interactions   -
XX
PS   Example 1; Page 39-40; 44pp; English.
XX
CC   The present sequence represents a mature FLINT (FAS Ligand Inhibitory
CC   Protein) polypeptide. The specification describers a composition
CC   comprising a divalent metal cation and FLINT protein. The composition
CC   is used either for reducing, reversing or eliminating aggregation and
CC   precipitation of FLINT or for inducing oligomerisation or aggregation
CC   of FLINT molecules. They can be used for purifying FLINT and/or
CC   maintaining FLINT in solution. The compositions are used to treat
CC   and/or prevent disorders associated with the binding of Fas to FasL
CC   and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the
CC   treatment of acute liver failure and cerebral ischemia and the prevention
CC   of apoptosis.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
```

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Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          ||||||||||||||||||||||||||||||||
Db    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
```

RESULT 8
AAB68047
ID AAB68047 standard; Protein; 271 AA.
XX
AC AAB68047;
XX
DT 29-JUN-2001 (first entry)
XX
DE Amino acid sequence of a human mature FLINT polypeptide.
XX
KW FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS Homo sapiens.
XX
PN WO200118041-A2.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-US20805.
XX
PR 10-SEP-1999; 99US-0153445.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Atkinson PR, Tian Y, Witcher DR;
XX
DR WPI; 2001-273381/28.
XX
PT Compositions comprising a divalent metal cation and a FAS Ligand
PT Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT FLINT and for treating diseases involving FasL/Fas and/or
PT LIGHT/LT-beta-R receptor interactions -
XX
PS Disclosure; Page 30-31; 33pp; English.
XX
CC The present sequence represents a human mature FLINT (FAS Ligand
CC Inhibitory Protein) polypeptide. The specification describers a
CC composition comprising a divalent metal cation and FLINT protein. The
CC composition is used either for reducing, reversing or eliminating
CC aggregation and precipitation of FLINT or for inducing oligomerisation
CC or aggregation of FLINT molecules. They can be used for purifying FLINT
CC and/or maintaining FLINT in solution. The compositions are used to treat
CC and/or prevent disorders associated with the binding of Fas to FasL
CC and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the
CC treatment of acute liver failure and cerebral ischemia and the prevention
CC of apoptosis.
XX
SQ Sequence 271 AA;

```
  Query Match            100.0%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity  100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy    121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy    181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          ||||||||||||||||||||||||||||||||
Db    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
```

RESULT 9
AAB74465
ID AAB74465 standard; protein; 271 AA.
XX
AC AAB74465;
XX
DT 30-MAY-2001 (first entry)
XX
DE Human FLINT mature protein.
XX
KW Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;
KW inflammatory disease.
XX
OS Homo sapiens.
XX
PN WO200118202-A2.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-US20806.
XX
PR 10-SEP-1999; 99US-0153433.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Atkinson PR, Tian Y, Witcher DR;
XX
DR WPI; 2001-257796/26.
XX
PT Compositions useful for reducing/inducing aggregation of a FLINT analog
PT comprise a divalent metal cation and a protease-resistant FAS Ligand
PT Inhibitory Protein (FLINT) analog -
XX
PS Claim 4; Page 41-42; 44pp; English.
XX
CC The present invention describes a composition comprising a divalent metal
CC cation associated with a protease resistant Fas ligand inhibitory protein
CC (FLINT) analogue. The composition is useful in the treatment of diseases
CC associated with Fas binding to its ligand, such as acute liver failure,
CC inflammatory diseases, cerebral ischaemia and apoptosis. The present
CC sequence is the mature FLINT protein.
XX
SQ Sequence 271 AA;

```
  Query Match            100.0%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity  100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy    121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy    181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
```

```
                                  ||||||||||||||||||||||||||||||
Db    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 10
AAE14578
ID   AAE14578 standard; Protein; 271 AA.
XX
AC   AAE14578;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human mature FLINT protein.
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human.
XX
OS   Homo sapiens.
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
DR   N-PSDB; AAD27868.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page 29-30; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analog.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   mature FLINT protein.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 23;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
           ||||||||||||||||||||||||||||||||
Db     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 11
AAW66102
ID   AAW66102 standard; Protein; 300 AA.
XX
AC   AAW66102;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Amino acid sequence of tumour necrosis related receptor (TR4).
XX
KW   Human; tumour necrosis related receptor; TR4; agonist; antagonist;
KW   inhibition; chronic; acute; inflammation; arthritis; septicaemia;
KW   autoimmune disease; transplant rejection; stroke; cancer;
KW   Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   EP861850-A1.
XX
PD   02-SEP-1998.
XX
PF   20-JAN-1998;   98EP-0300382.
XX
PR   04-FEB-1997;   97US-0794796.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Emery J,  Tan KB,  Truneh A,  Young PR;
XX
DR   WPI; 1998-508248/44.
DR   N-PSDB; AAV07654.
XX
PT   New DNA encoding tumour necrosis related receptor - used to treat
PT   and prevent e.g. inflammation, arthritis, septicaemia, autoimmune
PT   diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
PT   restenosis, AIDS, bone disorders and cancer
XX
PS   Claim 1; Fig 1; 21pp; English.
XX
CC   This is the amino acid sequence of the human tumour necrosis related
CC   receptor (TR4), used in the method of the invention.  The TR4 protein
CC   or its agonist can be used to treat a subject in need of enhanced
CC   TR4 polypeptide activity.  The antagonist is used to inhibit TR4
CC   polypeptide activity.  The active agents can be used for the
CC   treatment and prevention of diseases such as chronic and acute
CC   inflammation, arthritis, septicaemia, autoimmune diseases, transplant
CC   rejection, stroke, cancer, Alzheimer's disease.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1491;  DB 19;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
```

```
Qy    121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy    181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          |||||||||||||||||||||||||||||||
Db    270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

```
RESULT 12
AAW63622
ID   AAW63622 standard; Protein; 300 AA.
XX
AC   AAW63622;
XX
DT   26-OCT-1998  (first entry)
XX
DE   Human tumour necrosis factor receptor-6 alpha protein.
XX
KW   Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW   endothelial cells; keratinocytes; normal prostate; apoptosis;
KW   prostate tumour tissue.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT   Protein         31..300
FT                   /note= "TNFR-6 alpha"
FT   Region          31..282
FT                   /note= "Soluble extracellular domain"
XX
PN   WO9830694-A2.
XX
PD   16-JUL-1998.
XX
PF   13-JAN-1998;   98WO-US00153.
XX
PR   14-JAN-1997;   97US-0035496.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ebner R,  Feng P,  Gentz RL,  Ni J,  Ruben SM,  Yu G;
XX
DR   WPI; 1998-399142/34.
DR   N-PSDB; AAV39085.
XX
PT   Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
PT   the diagnosis of immune system-related disorder(s)
XX
PS   Claim 20; Fig 1; 91pp; English.
XX
CC   The present sequence represents the human tumour necrosis factor
CC   receptor-6 alpha (TNFR-6 alpha) protein.  The invention also provides
CC   for the TNFR-6 beta protein (AAW63623).  TNFR-6 alpha and TNFR-6 beta
CC   are members of the tumour necrosis factor receptor (TNFR) family.  TNFRs
CC   are expressed in endothelial cells, keratinocytes, normal prostate and
CC   prostate tumour tissue.  For a number of disorders of these cells,
CC   particularly of the immune system, substantially altered (whether
CC   increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
CC   expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
CC   polypeptides, nucleic acids and antibodies are claimed to be useful in
CC   the diagnosis of such disorders.  Mutations of the TNFR-6 alpha and
CC   TNFR-6 beta genes can also be detected.  The TNFR polypeptides are
CC   also claimed to be useful for identifying ligands which may be useful
CC   in the treatment of apoptosis related disorders.
XX
SQ   Sequence   300 AA;
```

```
  Query Match           100.0%;  Score 1491;  DB 19;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy    121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy    181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          |||||||||||||||||||||||||||||||
Db    270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

```
RESULT 13
AAY03099
ID   AAY03099 standard; Protein; 300 AA.
XX
AC   AAY03099;
XX
DT   09-DEC-1999  (first entry)
XX
DE   Human lung TNF-receptor protein.
XX
KW   Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;
KW   detection; immunoassay; diagnosis; disease; immune system; tumour;
KW   osteogenic system; cardiovascular system; central nervous system; asthma;
KW   peripheral nervous systems; transplant incompatibility; antitumor;
KW   rheumatoid arthritis; antiasthmatic; antiarthritic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             134..1036
FT                   /*tag=  a
FT                   /product= "TNF-receptor"
XX
PN   DE19809978-A1.
XX
PD   16-SEP-1999.
XX
PF   09-MAR-1998;   98DE-1009978.
XX
PR   09-MAR-1998;   98DE-1009978.
XX
PA   (BADI ) BASF AG.
XX
PI   Kroeger B;
XX
DR   WPI; 1999-519473/44.
DR   N-PSDB; AAZ09998.
XX
PT   New soluble member of tumor necrosis factor receptor family, useful for
PT   identification specific modulators and for treating disease e.g. tumors
PT    -
XX
PS   Claim 1; Page 8-9; 10pp; German.
XX
CC   This invention describes a novel tumour necrosis factor (TNF) receptor
CC   (I) isolated from human lung tissue. (I) is used: (i) to raise specific
CC   antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands
```

```
CC   (A), potential therapeutic agents; and (iii) therapeutically (optionally
CC   expressed from a gene therapy vector) in conditions associated with a
CC   deficit of (I). Ab are used: (a) for qualitative or quantitative
CC   detection of (I) in standard immunoassays (for diagnosis of disease, or
CC   susceptibility, or for monitoring); and (b) as therapeutic inhibitors in
CC   cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is
CC   used: (A) for recombinant production of (I); (B) also its oligonucleotide
CC   fragments, in standard hybridization and/or amplification assays; (C) as
CC   source of antisense molecules or ribozymes; and (D) to produce transgenic
CC   animals (for studying (patho)physiology of (I)). Diseases possibly
CC   associated with under- or over-expression of (I) are those of the immune,
CC   osteogenic, cardiovascular and central or peripheral nervous systems,
CC   tumors, transplant incompatibility, asthma and rheumatoid arthritis. The
CC   products of the invention have antitumor, antiasthmatic and
CC   antiarthritic activity. This sequence represents the TNF-receptor of the
CC   invention.
XX
SQ   Sequence   300 AA;

  Query Match            100.0%;  Score 1491;  DB 20;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          |||||||||||||||||||||||||||||||
Db     270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 14
AAY42182
ID   AAY42182 standard; Protein; 300 AA.
XX
AC   AAY42182;
XX
DT   17-DEC-1999  (first entry)
XX
DE   Human FLINT #1 protein sequence.
XX
KW   Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW   apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW   sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW   reperfusion-associated injury; aplastic anaemia; differentiation;
KW   growth; myelodysplastic syndrome; pancytopenic condition;
KW   myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO9950413-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06797.
XX
PR   30-MAR-1998;   98US-0079856.
PR   20-MAY-1998;   98US-0086074.
PR   09-SEP-1998;   98US-0099643.
PR   17-DEC-1998;   98US-0112577.
PR   18-DEC-1998;   98US-0112703.
PR   18-DEC-1998;   98US-0112933.
PR   22-DEC-1998;   98US-0113407.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bumol TF,  Dou S,  Glasebrook AL,  Gould KE,  Hale JE,  Heuer JG;
PI   Hui KY,  Kharitonenkov A,  Mizrahi J,  Na S,  Noblitt TW,  Reidy CA;
PI   Song HY,  Wang J,  Wu X,  Zuckerman SH;
XX
DR   WPI; 1999-591319/50.
DR   N-PSDB; AAZ25375.
XX
PT   Use of mature FLINT for treating acute liver failure, inflammation,
PT   cancer, and diabetes  - by prevention of FasL-Fas mediated apoptotic
PT   and proinflammatory activity
XX
PS   Claim 30; Fig 1; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   represents human FLINT.
XX
SQ   Sequence   300 AA;

  Query Match            100.0%;  Score 1491;  DB 20;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-115;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
          |||||||||||||||||||||||||||||||
Db     270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 15
AAY17479
ID   AAY17479 standard; Protein; 300 AA.
XX
AC   AAY17479;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Mammalian tumour necrosis factor receptor OPG-2.
```

XX
KW Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;
KW osteopenic disorder; osteoclast activity; primary osteoporosis;
KW hyperglycaemia; osteolytic metastasis; immune response; cancer.
XX
OS Mammalia.
XX
PN WO9926977-A1.
XX
PD 03-JUN-1999.
XX
PF 24-NOV-1998; 98WO-US25065.
XX
PR 17-FEB-1998; 98US-0074896.
PR 24-NOV-1997; 97US-0066446.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Tschopp J;
XX
DR WPI; 1999-347693/29.
DR N-PSDB; AAX76052.
XX
PT New tumour necrosis factor family receptor OPG-2
XX
PS Claim 1; Page 18; 22pp; English.
XX
CC The present sequence represents a mammalian tumour necrosis factor
CC receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis
CC factor receptor family, and can be used: (i) to raise specific
CC antibodies (Ab), (ii) to treat osteopenic disorders associated with
CC excessive osteoclast activity, e.g. primary osteoporosis, Paget's
CC disease; hyperglycaemia of malignancy, or osteolytic metastases; (iii)
CC for affinity purification of cognate ligands, and (iv) to screen for
CC ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents
CC such as soluble forms of the protein, are used to prevent, or reduce
CC severity of, an immune response, and for treating cancer. They can also
CC be used in diagnostic assays. The nucleic acid sequence encoding OPG-2
CC can be used as a probe to isolate related sequences from other species.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 9.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
           |||||||||||||||||||||||||||||||
Db     270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
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Search completed: January 6, 2003, 11:16:50
Job time : 63 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 11:16:55 ; Search time 21 Seconds
(without alignments)
379.696 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1491	100.0	300	2	US-08-794-796-2	Sequence 2, Appli
2	1476.5	99.0	299	4	US-09-286-529-17	Sequence 17, Appl
3	1034	69.3	211	4	US-09-286-529-20	Sequence 20, Appl
4	841	56.4	153	4	US-09-286-529-2	Sequence 2, Appli
5	440.5	29.5	401	3	US-08-974-022-6	Sequence 6, Appli
6	440.5	29.5	401	4	US-09-042-785A-12	Sequence 12, Appl
7	440.5	29.5	401	4	US-08-795-445A-6	Sequence 6, Appli
8	440.5	29.5	401	4	US-08-795-447A-6	Sequence 6, Appli
9	440.5	29.5	401	4	US-08-974-186-6	Sequence 6, Appli
10	440.5	29.5	401	4	US-08-795-446B-6	Sequence 6, Appli
11	440.5	29.5	401	4	US-09-153-927-1	Sequence 1, Appli
12	440.5	29.5	401	4	US-09-072-993C-1	Sequence 1, Appli
13	440.5	29.5	401	4	US-08-706-945D-128	Sequence 128, App
14	425.5	28.5	401	3	US-08-974-022-2	Sequence 2, Appli
15	425.5	28.5	401	4	US-08-795-445A-2	Sequence 2, Appli
16	425.5	28.5	401	4	US-08-795-447A-2	Sequence 2, Appli
17	425.5	28.5	401	4	US-08-974-186-2	Sequence 2, Appli
18	425.5	28.5	401	4	US-08-795-446B-2	Sequence 2, Appli
19	425.5	28.5	401	4	US-08-706-945D-124	Sequence 124, App
20	424.5	28.5	401	3	US-08-974-022-4	Sequence 4, Appli
21	424.5	28.5	401	4	US-09-042-785A-13	Sequence 13, Appl
22	424.5	28.5	401	4	US-08-795-445A-4	Sequence 4, Appli
23	424.5	28.5	401	4	US-08-795-447A-4	Sequence 4, Appli
24	424.5	28.5	401	4	US-08-974-186-4	Sequence 4, Appli
25	424.5	28.5	401	4	US-08-795-446B-4	Sequence 4, Appli
26	424.5	28.5	401	4	US-08-706-945D-126	Sequence 126, App
27	407	27.3	147	4	US-09-527-236A-20	Sequence 20, Appl
28	394	26.4	174	4	US-08-706-945D-136	Sequence 136, App
29	385.5	25.9	364	4	US-08-706-945D-142	Sequence 142, App
30	374.5	25.1	364	4	US-08-706-945D-141	Sequence 141, App
31	373	25.0	139	4	US-08-706-945D-130	Sequence 130, App
32	342.5	23.0	461	4	US-09-042-785A-7	Sequence 7, Appli
33	342.5	23.0	461	4	US-09-006-353A-4	Sequence 4, Appli
34	342.5	23.0	461	4	US-09-573-986-4	Sequence 4, Appli
35	340.5	22.8	461	1	US-08-385-229-2	Sequence 2, Appli
36	340.5	22.8	461	2	US-08-650-000-2	Sequence 2, Appli
37	340.5	22.8	461	4	US-08-477-347-3	Sequence 3, Appli
38	340.5	22.8	461	4	US-08-476-862-2	Sequence 2, Appli
39	340.5	22.8	461	6	5395760-2	Patent No. 5395760
40	335	22.5	227	3	US-08-974-022-48	Sequence 48, Appl
41	335	22.5	227	4	US-08-795-445A-48	Sequence 48, Appl
42	335	22.5	227	4	US-08-795-447A-48	Sequence 48, Appl
43	335	22.5	227	4	US-08-974-186-48	Sequence 48, Appl
44	335	22.5	227	4	US-08-795-446B-48	Sequence 48, Appl
45	335	22.5	227	4	US-08-706-945D-134	Sequence 134, App

ALIGNMENTS

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RESULT 1
US-08-794-796-2
; Sequence 2, Application US/08794796
; Patent No. 5885800
;  GENERAL INFORMATION:
;    APPLICANT:  Emery, John
;    APPLICANT:  Tan, KB
;    APPLICANT:  Truneh, Alem
;    APPLICANT:  Young, Peter
;    TITLE OF INVENTION:  Tumor Necrosis Related Receptor,
;    TITLE OF INVENTION:  TR4
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/794,796
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Han, William T
;      REGISTRATION NUMBER:  34,344
;      REFERENCE/DOCKET NUMBER:  GH50000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5219
;      TELEFAX:  610-270-4026
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  300 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-794-796-2

  Query Match           100.0%;  Score 1491;  DB 2;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 3e-124;
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  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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Db      30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
           |||||||||||||||||||||||||||||||
Db     270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 2
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-286-529-17

  Query Match             99.0%;  Score 1476.5;  DB 4;  Length 299;
  Best Local Similarity   99.6%;  Pred. No. 5.7e-123;
  Matches  270;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 CQPCPPGTFSA-SSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 208

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 268

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
           |||||||||||||||||||||||||||||||
Db     269 GALLVRLLQALRVARMPGLERSVRERFLPVH 299


RESULT 3
US-09-286-529-20
; Sequence 20, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 20
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-286-529-20

  Query Match             69.3%;  Score 1034;  DB 4;  Length 211;
  Best Local Similarity   98.9%;  Pred. No. 4.8e-84;
  Matches  179;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGEP 209

Qy     181 E 181
           |
Db     210 E 210


RESULT 4
US-09-286-529-2
; Sequence 2, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: human
US-09-286-529-2

  Query Match             56.4%;  Score 841;  DB 4;  Length 153;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-67;
  Matches  153;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      56 LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTP 115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTP 60

Qy     116 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 120

Qy     176 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 208
           |||||||||||||||||||||||||||||||||
Db     121 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 153


RESULT 5
US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
```

```
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,022
;      FILING DATE:  12-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-022-6

  Query Match             29.5%;  Score 440.5;  DB 3;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 2.9e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
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Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209


RESULT 6
US-09-042-785A-12
; Sequence 12, Application US/09042785A
; Patent No. 6194151
;  GENERAL INFORMATION:
;    APPLICANT:  Busfield, Samantha J
;    TITLE OF INVENTION:  NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
;    TITLE OF INVENTION:  AND USES THEREFOR
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,785A
;      FILING DATE:  17-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/938,896
;      FILING DATE:  26-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MEI-001CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-09-042-785A-12

  Query Match             29.5%;  Score 440.5;  DB 4;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 2.9e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||  :|:| :||||:::: |     | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
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Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
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Db     203 EEAFFRF 209


RESULT 7
US-08-795-445A-6
; Sequence 6, Application US/08795445A
; Patent No. 6284485
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,445A
;      FILING DATE:
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;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-445A-6

  Query Match             29.5%;  Score 440.5;  DB 4;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 2.9e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |    | ||  :|:| :|||||:::: |      | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209


RESULT 8
US-08-795-447A-6
; Sequence 6, Application US/08795447A
; Patent No. 6284728
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, William J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  Osteoprotegerin
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  One Amgen Center Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91362-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,447A
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378D2
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-447A-6

  Query Match             29.5%;  Score 440.5;  DB 4;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 2.9e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |    | ||  :|:| :|||||:::: |      | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209


RESULT 9
US-08-974-186-6
; Sequence 6, Application US/08974186
; Patent No. 6284740
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-186-6

  Query Match             29.5%;  Score 440.5;  DB 4;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 2.9e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |    | ||  :|:| :|||||:::: |      | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
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Db     86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy    125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
          | | ||  :||   |: | ||:  || |    |:::|| :   |:|   ||:  | :  |
Db    146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy    183 ERAVIDF 189
          | |   |
Db    203 EEAFFRF 209


RESULT 10
US-08-795-446B-6
; Sequence 6, Application US/08795446B
; Patent No. 6288032
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,446B
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-446B-6

  Query Match             29.5%;  Score 440.5;  DB 4;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 2.9e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy      5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
          | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db     26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy     65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
          :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db     86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy    125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
          | | ||  :||   |: | ||:  || |    |:::|| :   |:|   ||:  | :  |
Db    146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy    183 ERAVIDF 189
          | |   |
Db    203 EEAFFRF 209


RESULT 11
US-09-153-927-1
; Sequence 1, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
;  APPLICANT: McDonnell, Peter C.
;  APPLICANT: Young, Peter R.
;  APPLICANT: Zou, Jun
;  TITLE OF INVENTION: A Method of Identifying Agonists and
;  TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
;  TITLE OF INVENTION: and TR5
;  FILE REFERENCE: GH50031
;  CURRENT APPLICATION NUMBER: US/09/153,927A
;  CURRENT FILING DATE: 1998-09-16
;  EARLIER APPLICATION NUMBER: 60/061,334
;  EARLIER FILING DATE: 1997-10-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 401
;   TYPE: PRT
;   ORGANISM: Human
US-09-153-927-1

  Query Match             29.5%;  Score 440.5;  DB 4;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 2.9e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy      5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
          | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db     26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy     65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
          :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db     86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy    125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
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Db    146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy    183 ERAVIDF 189
          | |   |
Db    203 EEAFFRF 209


RESULT 12
US-09-072-993C-1
; Sequence 1, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
;  APPLICANT: Michael R. Brigham-Burke
;  APPLICANT:  Peter R. Young
;  TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
;  TITLE OF INVENTION:  ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
;  FILE REFERENCE: GH-50030
;  CURRENT APPLICATION NUMBER: US/09/072,993C
;  CURRENT FILING DATE:  1998-05-06
;  PRIOR APPLICATION NUMBER: 60/055,513
;  PRIOR FILING DATE: 1997-08-13
;  PRIOR APPLICATION NUMBER: 60/056,980
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/057,550
;  PRIOR FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 401
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-072-993C-1

  Query Match             29.5%;  Score 440.5;  DB 4;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 2.9e-31;
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  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
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Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209


RESULT 13
US-08-706-945D-128
; Sequence 128, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Lacey, David
;  APPLICANT:  Calzone, Frank
;  APPLICANT:  Chang, Ming-Shi
;  TITLE OF INVENTION: Osteoprotegerin
;  FILE REFERENCE: A-378CIP
;  CURRENT APPLICATION NUMBER: US/08/706,945D
;  CURRENT FILING DATE:  1996-09-03
;  PRIOR APPLICATION NUMBER: 08/577,788
;  PRIOR FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 145
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
;   LENGTH: 401
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-706-945D-128

  Query Match             29.5%;  Score 440.5;  DB 4;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 2.9e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |    | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209


RESULT 14
US-08-974-022-2
; Sequence 2, Application US/08974022
; Patent No. 6015938
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,022
;      FILING DATE:  12-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-022-2

  Query Match             28.5%;  Score 425.5;  DB 3;  Length 401;
  Best Local Similarity   39.5%;  Pred. No. 6.2e-30;
  Matches   81;  Conservative   33;  Mismatches   86;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |    | ||| :|:| :| |||:::: |     | | |||    ||  |:  : | ||:
Db      26 PKYLHYDPETGRQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDYSYTDSWHTSDECVYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |  | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQTVKQECNRTHNRVCECEEGRYLELEFCLKHRSCPPGLGVLQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||::||| |    |:::|| :   |:|   :|:  | :   |
Db     146 PDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNV---CSGNREATQNCGIDVTLC 202

Qy     183 ERAVIDFVAFQDISIKRLQRLLQAL 207
           | |   |     |    |  |: :|
Db     203 EEAFFRFAVPTKIIPNWLSVLVDSL 227


RESULT 15
US-08-795-445A-2
; Sequence 2, Application US/08795445A
; Patent No. 6284485
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/795,445A
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/577,788
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Winter, Robert B.
;       REFERENCE/DOCKET NUMBER:  A-378
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  401 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-795-445A-2

  Query Match             28.5%;  Score 425.5;  DB 4;  Length 401;
  Best Local Similarity   39.5%;  Pred. No. 6.2e-30;
  Matches   81;  Conservative   33;  Mismatches   86;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||| :|:| :| |||:::: |     | | |||   ||  |:  : | ||:
Db      26 PKYLHYDPETGRQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDYSYTDSWHTSDECVYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |  | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQTVKQECNRTHNRVCECEEGRYLELEFCLKHRSCPPGLGVLQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
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Db     146 PDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNV---CSGNREATQNCGIDVTLC 202

Qy     183 ERAVIDFVAFQDISIKRLQRLLQAL 207
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Db     203 EEAFFRFAVPTKIIPNWLSVLVDSL 227


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GenCore version 5.1.3
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1491	100.0	813	20	AAZ25377	Human mFLINT #1 nu
2	1491	100.0	813	21	AAA75999	DNA encoding a mat
3	1491	100.0	813	21	AAA88730	Human FAS ligand i
4	1491	100.0	813	21	AAA51077	Mature human FLINT
5	1491	100.0	813	22	AAD07380	Human mature fas l
6	1491	100.0	813	24	AAD27868	Human mature FLINT
7	1491	100.0	900	20	AAZ25375	Human FLINT #1 nuc
8	1491	100.0	900	21	AAA53208	Human Fas ligand i
9	1491	100.0	900	21	AAA51075	Human FLINT coding
10	1491	100.0	903	20	AAX22300	Orphan receptor (H
11	1491	100.0	903	24	AAD33295	Mammalian syntheti
12	1491	100.0	1055	22	AAF62705	Human NTR3 nucleot
13	1491	100.0	1066	21	AAA53802	M68 TNF receptor r
14	1491	100.0	1077	19	AAV39085	Human tumour necro
15	1491	100.0	1077	21	AAA37772	Human tumour necro
16	1491	100.0	1077	24	AAD33281	Human tumour necro
17	1491	100.0	1114	20	AAX32744	Human DcR3 polypep
18	1491	100.0	1114	21	AAC58367	Human PRO212 nucle
19	1491	100.0	1114	21	AAC58581	Human PRO212 prote
20	1491	100.0	1114	21	AAA77537	Human PRO212 cDNA
21	1491	100.0	1114	22	AAC84421	Human PRO212 polyp
22	1491	100.0	1114	22	AAC91462	Human PRO212 cDNA.
23	1491	100.0	1164	19	AAV07654	Nucleotide sequenc
24	1491	100.0	1168	20	AAZ09998	Human lung TNF-rec
25	1491	100.0	1179	22	AAH33171	Human colon cancer
26	1491	100.0	1205	20	AAX07226	Human tumour necro
27	1491	100.0	1347	21	AAC63764	Human soluble TNF
28	1491	100.0	1428	21	AAA53801	M68 TNF receptor r
29	1491	100.0	1462	20	AAX76052	Mammalian tumour n
30	1491	100.0	1550	24	AAD33296	Codon optimised tu
31	1485	99.6	825	20	AAZ25378	Human mFLINT #2 nu
32	1485	99.6	825	21	AAA51078	Human mature FLINT
33	1485	99.6	936	20	AAZ25376	Human FLINT #2 nuc
34	1477	99.1	1137	21	AAZ92404	cDNA encoding huma
35	1476	99.0	936	21	AAA88731	Human FAS ligand i
36	1476	99.0	936	21	AAA51076	Human FLINT coding
37	1476	99.0	936	22	AAD07385	Human fas ligand i
38	1476	99.0	936	22	AAF89920	Nucleotide sequenc
39	1476	99.0	936	22	AAF84738	Nucleotide sequenc
40	1476	99.0	936	22	AAF84739	Nucleotide sequenc
41	1476	99.0	936	22	AAF77696	Human FLINT native
42	1476	99.0	936	24	AAD27869	Human FLINT analog
43	1459.5	97.9	1224	24	ABQ55057	Human ovarian anti
44	1384	92.8	900	21	AAA53209	Monkey Fas ligand
45	1339	89.8	1859	21	AAC63765	Human soluble TNF

ALIGNMENTS

RESULT 1
AAZ25377
ID AAZ25377 standard; cDNA; 813 BP.
XX
AC AAZ25377;
XX
DT 17-DEC-1999 (first entry)
XX
DE Human mFLINT #1 nucleotide sequence.
XX
KW Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancytopenic condition;
KW myocardial ischaemia; ss.
XX
OS Homo sapiens.

XX
PN WO9950413-A2.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US06797.
XX
PR 30-MAR-1998; 98US-0079856.
PR 20-MAY-1998; 98US-0086074.
PR 09-SEP-1998; 98US-0099643.
PR 17-DEC-1998; 98US-0112577.
PR 18-DEC-1998; 98US-0112703.
PR 18-DEC-1998; 98US-0112933.
PR 22-DEC-1998; 98US-0113407.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
PI Hui KY, Kharitonenkov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
PI Song HY, Wang J, Wu X, Zuckerman SH;
XX
DR WPI; 1999-591319/50.
DR P-PSDB; AAZ42184.
XX
PT Use of mature FLINT for treating acute liver failure, inflammation,
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
PT and proinflammatory activity
XX
PS Claim 29; Fig 3; 99pp; English.
XX
CC The present invention describes therapeutic applications of mature FLINT
CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC (mFLINT), which is a member of the tumour necrosis factor receptor
CC superfamily, is used for treating acute liver failure, inflammation of
CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC injury or disorder such as hypercoagulation (including use with
CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC or disorder, Type I diabetes, cancer, cell damage or damage to an
CC innocent bystander tissue that is induced by a chemotherapeutic agent or
CC therapeutic irradiation, treating haematopoietic progenitor cells that
CC have been exposed to therapeutic radiation or chemotherapy, aplastic
CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC also used for promoting the growth or differentiation of a haematopoietic
CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC resulting from abnormal myocardial ischaemia. The present sequence
CC encodes human mFLINT.
XX
SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:

Pred. No.:	3.46e-77	Length:	813
Score:	1491.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-936-024-1 (1-271) x AAZ25377 (1-813)

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Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

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Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
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Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    161 AspThrLeuCysThrSerCysThrGlyProLeuSerThrArgValProGlyAlaGlu 180
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Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
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Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
```

RESULT 2
AAA75999
ID AAA75999 standard; DNA; 813 BP.
XX
AC AAA75999;
XX
DT 19-FEB-2001 (first entry)
XX
DE DNA encoding a mature human FAS Ligand Inhibitory Protein (FLINT).
XX
KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW acute respiratory distress syndrome; ulcerative colitis;
KW chronic obstructive pulmonary disease; Crohn's disease; ss.
XX
OS Homo sapiens.
XX
PN WO200058465-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000WO-US06417.
XX
PR 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140077.
PR 21-JUN-1999; 99US-0140156.
PR 20-OCT-1999; 99US-0160566.
PR 18-FEB-2000; 2000US-0183398.
XX
PA (ELIL) LILLY & CO ELI.

```
XX
PI   Becker GW,  Cohen FJ,  Gonzalez-dewhitt PA,  Hale JE,  Micanovic R;
PI   Newton CM,  Noblitt TW,  Rathmachalam R,  Tschang SR,  Witcher DR;
PI   Wroblewski VJ;
XX
DR   WPI; 2000-656167/63.
DR   P-PSDB; AAB19334.
XX
PT   FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT   apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT   chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT   disease  -
XX
PS   Claim 37; Page 113; 114pp; English.
XX
CC   The present sequence encodes a mature human FAS Ligand Inhibitory
CC   Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC   proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC   FLINT protein is modified to produce analogues, which have greater
CC   potency, longer in vivo half-lives, decreased aggregation, decreased
CC   absorption onto surfaces, increased solubility and improved ease of
CC   formulation. The FLINT analogue is useful for treating a patient
CC   suffering from disease or condition relating to abnormal apoptosis such
CC   as acute lung injury, acute respiratory distress syndrome, pulmonary
CC   fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC   Crohn's disease.
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:
Pred. No.:              3.46e-77      Length:         813
Score:                  1491.00       Matches:        271
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     21            Gaps:           0

US-09-936-024-1 (1-271) x AAA75999 (1-813)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Db      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Db     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy     161 AspThrLeuCysThrSerCysThrGlyProProLeuSerThrArgValProGlyAlaGlu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Db     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
           |||||||||||||||||||||||||||||||
Db     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813

RESULT 3
AAA88730
ID   AAA88730 standard; cDNA; 813 BP.
XX
AC   AAA88730;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Human FAS ligand inhibitor protein FLINT cDNA.
XX
KW   FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW   acute lung injury; acute respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   ulcerative colitis; therapy; organ transpantation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058466-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06418.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140073.
PR   04-AUG-1999;   99US-0147071.
PR   20-OCT-1999;   99US-0160524.
PR   21-OCT-1999;   99US-0160669.
PR   20-DEC-1999;   99US-0172744.
PR   26-JAN-2000; 2000US-0178184.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Rathnachalam R,  Witcher DR;
XX
DR   WPI; 2000-664925/64.
DR   P-PSDB; AAB19705.
XX
PT   Novel protease resistant FAS ligand inhibitory protein analogues
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases  -
XX
PS   Disclosure; Page 95; 100pp; English.
XX
CC   The present sequence is that of cDNA coding for human FAS ligand
CC   inhibitory protein FLINT mature protein (see AAB19705).  FLINT is a
CC   tumour necrosis factor receptor homologue that binds FAS ligand,
CC   preventing its interaction with FAS.  This interaction is implicated
CC   in runaway apoptosis and inflammatory disease.  FLINT also binds to
CC   LIGHT, a membrane-bound ligand, which may play a role in immune
CC   modulation and apoptosis.  The invention relates to novel FLINT
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CC   analogues (see also AAB19706-09) that are resistant to proteolysis
CC   by trypsin-like proteases between positions 218 and 219 of the
CC   FLINT mature protein sequence.  Nucleic acids, vectors and
CC   transformed host cells for recombinant production of the analogues
CC   are claimed.  FLINT cDNA is used as a template for introducing the
CC   required point mutations e.g. via PCR mutagenesis.  The protease
CC   resistant FLINT analogues are used to prevent or treat acute lung
CC   injury, acute respiratory stress syndrome, ulcerative colitis,
CC   chronic obstructive pulmonary disease, pulmonary fibrosis, to
CC   inhibit T lymphocyte activation, and to facilitate organ
CC   preservation for transplantation (claimed).
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:
Pred. No.:                3.46e-77       Length:          813
Score:                    1491.00        Matches:         271
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       21             Gaps:            0

US-09-936-024-1 (1-271) x AAA88730 (1-813)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813

RESULT 4
AAA51077
ID   AAA51077 standard; DNA; 813 BP.
XX
AC   AAA51077;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Mature human FLINT coding sequence.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     1..813
FT                   /*tag=  a
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   P-PSDB; AAY96598.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 8; Fig 3A-B; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:
Pred. No.:                3.46e-77       Length:          813
Score:                    1491.00        Matches:         271
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
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Query Match:            100.00%       Indels:        0
DB:                     21            Gaps:          0

US-09-936-024-1 (1-271) x AAA51077 (1-813)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Db     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
           ||||||||||||||||||||||||||||||||
Db     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813

RESULT 5
AAD07380
ID   AAD07380 standard; cDNA; 813 BP.
XX
AC   AAD07380;
XX
DT   04-AUG-2001  (first entry)
XX
DE   Human mature fas ligand inhibitory protein (FLINT) cDNA.
XX
KW   Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
KW   TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KW   acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KW   chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
KW   rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
KW   fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KW   chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KW   vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KW   insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KW   Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KW   Down's syndrome; multiple sclerosis; cytostatic; nootropic;
KW   neuroprotective; vasotropic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..813
FT                   /*tag=  a
FT                   /product= "Human mature fas ligand inhibitory protein
FT                   (FLINT)"
FT                   /note= "CDS does not include start and stop codon"
FT                   /partial
XX
PN   WO200142463-A1.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US30166.
XX
PR   07-DEC-1999;   99US-0169367.
PR   07-DEC-1999;   99US-0169381.
PR   07-DEC-1999;   99US-0169412.
PR   23-MAR-2000; 2000US-0191430.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Lu J,  Witcher DR;
XX
DR   WPI; 2001-381684/40.
DR   P-PSDB; AAE03567.
XX
PT   New FLINT polypeptide for treating and/or preventing acute lung injury,
PT   acute respiratory distress syndrome, ulcerative colitis, and
PT   graft-versus-host disease, comprises O-linked or N-linked
PT   oligosaccharides -
XX
PS   Example 1; Page 53; 60pp; English.
XX
CC   The present sequence is human mature fas ligand inhibitory protein
CC   (FLINT) cDNA. FLINT, a homologue of tumour necrosis factor receptor
CC   protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC   interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC   oligosaccharides is useful for preventing or treating acute lung injury
CC   (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC   chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC   to facilitate organ preservation for transplantation and to inhibit T
CC   lymphocyte activation. FLINT is useful for treating and/or preventing
CC   diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC   fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC   (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC   host disease, cutaneous inflammation, vascular leak syndrome,
CC   Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC   diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC   Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC   psoriasis, Down's syndrome, and multiple sclerosis.
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:
Pred. No.:              3.46e-77        Length:         813
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     22              Gaps:           0
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US-09-936-024-1 (1-271) x AAD07380 (1-813)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
           ||||||||||||||||||||||||||||||||
Db     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
```

```
RESULT 6
AAD27868
ID   AAD27868 standard; DNA; 813 BP.
XX
AC   AAD27868;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human mature FLINT DNA.
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..813
FT                   /*tag=  a
FT                   /product= "Mature FLINT protein"
FT                   /note= "Does not include start and stop codons"
FT                   /partial
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
DR   P-PSDB; AAE14578.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page 30; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analog.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   mature FLINT DNA.
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
```

```
Alignment Scores:
Pred. No.:                3.46e-77        Length:          813
Score:                    1491.00         Matches:         271
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       24              Gaps:            0

US-09-936-024-1 (1-271) x AAD27868 (1-813)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    161 AspThrLeuCysThrSerCysThrGlyProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
```

RESULT 7
AAZ25375
ID AAZ25375 standard; cDNA; 900 BP.
XX
AC AAZ25375;
XX
DT 17-DEC-1999 (first entry)
XX
DE Human FLINT #1 nucleotide sequence.
XX
KW Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancytopenic condition;
KW myocardial ischaemia; ss.
XX
OS Homo sapiens.
XX
PN WO9950413-A2.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US06797.
XX
PR 30-MAR-1998; 98US-0079856.
PR 20-MAY-1998; 98US-0086074.
PR 09-SEP-1998; 98US-0099643.
PR 17-DEC-1998; 98US-0112577.
PR 18-DEC-1998; 98US-0112703.
PR 18-DEC-1998; 98US-0112933.
PR 22-DEC-1998; 98US-0113407.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
PI Hui KY, Kharitonenkov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
PI Song HY, Wang J, Wu X, Zuckerman SH;
XX
DR WPI; 1999-591319/50.
DR P-PSDB; AAY42182.
XX
PT Use of mature FLINT for treating acute liver failure, inflammation,
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
PT and proinflammatory activity
XX
PS Claim 28; Fig 1; 99pp; English.
XX
CC The present invention describes therapeutic applications of mature FLINT
CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC (mFLINT), which is a member of the tumour necrosis factor receptor
CC superfamily, is used for treating acute liver failure, inflammation of
CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC injury or disorder such as hypercoagulation (including use with
CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC or disorder, Type I diabetes, cancer, cell damage or damage to an
CC innocent bystander tissue that is induced by a chemotherapeutic agent or
CC therapeutic irradiation, treating haematopoietic progenitor cells that
CC have been exposed to therapeutic radiation or chemotherapy, aplastic
CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC also used for promoting the growth or differentiation of a haematopoietic
CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC resulting from abnormal myocardial ischaemia. The present sequence
CC encodes human FLINT.
XX
SQ Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

Alignment Scores:

Pred. No.:	3.85e-77	Length:	900
Score:	1491.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-936-024-1 (1-271) x AAZ25375 (1-900)

```
Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db    448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db    868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900

RESULT 8
AAA53208
ID   AAA53208 standard; cDNA; 900 BP.
XX
AC   AAA53208;
XX
DT   03-JAN-2001  (first entry)
XX
DE   Human Fas ligand inhibitor FLINT coding sequence.
XX
KW   Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
KW   inflammation; infectious disease; ischaemia; Alzheimer's disease;
KW   Parkinson's disease; Crohn's disease; transplantation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..900
FT                   /*tag=  a
FT                   /product= "FLINT"
FT                   /partial
FT   sig_peptide     1..90
FT                   /*tag=  b
FT   mat_peptide     91..900
FT                   /*tag=  c
XX
PN   WO200034782-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-US28696.
XX
PR   09-DEC-1998;   98US-0111575.
PR   09-DEC-1998;   98US-0111580.
PR   07-JAN-1999;   99US-0115069.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Rosteck PRJ,  Song HY,  Su EW;
XX
DR   WPI; 2000-431379/37.
DR   P-PSDB; AAB03621.
XX
PT   Novel monkey Fas ligand inhibitor polypeptides, useful for treating
PT   inflammatory or autoimmune disease such as rheumatoid arthritis,
PT   infectious diseases such as chronic hepatitis, and
PT   Ischaemia/Re-perfusion conditions -
XX
PS   Example 1; Page 88-91; 101pp; English.
XX
CC   The present sequence is the coding sequence of the human Fas ligand
CC   inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC   apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC   such as rheumatoid arthritis, inflammatory bowel disease,
CC   graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC   infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC   hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC   ulceration, ischaemia and reperfusion conditions including acute
CC   myocardial infarction, acute coronary syndrome, congestive heart failure
CC   and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung
CC   injury and acute respiratory distress syndrome, Crohn's disease, brain
CC   trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic
CC   anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
CC   multiple sclerosis. In addition, the gene and protein can be used to
CC   prevent apoptosis following organ transplantation.
XX
SQ   Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

Alignment Scores:
Pred. No.:                3.85e-77        Length:          900
Score:                    1491.00         Matches:         271
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       21              Gaps:            0

US-09-936-024-1 (1-271) x AAA53208 (1-900)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis.160
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Db    508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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Db    568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db    868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900

RESULT 9
AAA51075
ID   AAA51075 standard; DNA; 900 BP.
XX
AC   AAA51075;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human FLINT coding sequence.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..900
FT                   /*tag=  a
FT                   /product= FLINT
FT                   /partial
FT   sig_peptide     1..87
FT                   /*tag=  b
FT   mat_peptide     88..900
FT                   /*tag=  c
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   P-PSDB; AAY96596.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 7; Fig 1A-B; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction..Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

Alignment Scores:
Pred. No.:              3.85e-77        Length:         900
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     21              Gaps:           0

US-09-936-024-1 (1-271) x AAA51075 (1-900)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db    268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy    161 AspThrLeuCysThrSerCysThrGlyProProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867
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```
Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          ||||||||||||||||||||||||||||||||
Db    868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900

RESULT 10
AAX22300
ID   AAX22300 standard; DNA; 903 BP.
XX
AC   AAX22300;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.
XX
KW   HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
KW   tumour necrosis factor receptor; muscle disorder; bone mass; screening;
KW   muscle metabolism; binding agent; cognate ligand; ss.
XX
OS   Homo sapiens.
XX
PN   WO9907738-A2.
XX
PD   18-FEB-1999.
XX
PF   04-AUG-1998;   98WO-US16202.
XX
PR   06-AUG-1997;   97US-0054869.
XX
PA   (PROC ) PROCTER & GAMBLE CO.
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Masiakowski PJ,  Morris J,  Valenzuela DM;
XX
DR   WPI; 1999-167365/14.
DR   P-PSDB; AAW95082.
XX
PT   Novel orphan human receptor polypeptide and nucleic acid - useful as
PT   diagnostic reagents and for treatment of muscle disorders
XX
PS   Claim 2; Page 21; 23pp; English.
XX
CC   This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The
CC   protein is related to osteoprotegerin (OPG) and to tumour necrosis factor
CC   receptor (TNFR). Host cells transformed with a vector comprising the
CC   HUMAN NTR-1 nucleic acid are used for the recombinant expression of the
CC   protein. HUMAN NTR-1 proteins and antibodies immuno specific for the
CC   protein are useful for diagnosis and treatment of humans and animals,
CC   especially muscle disorders, as the receptor is involved in regulation of
CC   bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful
CC   for screening for novel binding agents, and cognate ligands, which may be
CC   used to treat disorders associated with HUMAN NTR-1 imbalance.
XX
SQ   Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;

Alignment Scores:
Pred. No.:               3.86e-77      Length:          903
Score:                   1491.00       Matches:         271
Percent Similarity:      100.00%       Conservative:    0
Best Local Similarity:   100.00%       Mismatches:      0
Query Match:             100.00%       Indels:          0
DB:                      20            Gaps:            0

US-09-936-024-1 (1-271) x AAX22300 (1-903)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db     88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          ||||||||||||||||||||||||||||||||
Db    868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900

RESULT 11
AAD33295
ID   AAD33295 standard; DNA; 903 BP.
XX
AC   AAD33295;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Mammalian synthetic tumour necrosis factor receptor (TNFR)-6alpha DNA.
XX
KW   Tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;
KW   immune system-related disorder; inflammatory disease; immunosuppressive;
KW   bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;
KW   autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW   multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;
KW   graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;
KW   neuroprotective; antiarteriosclerotic; dermatological; asthma; receptor;
KW   gene; ds.
XX
OS   Mammalia.
OS   Synthetic.
XX
PN   WO200218622-A2.
XX
PD   07-MAR-2002.
```

XX
PF 24-AUG-2001; 2001WO-US26396.
XX
PR 25-AUG-2000; 2000US-227598P.
PR 21-NOV-2000; 2000US-252131P.
PR 06-JUL-2001; 2001US-303224P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Gentz RL, Ebner R, Yu G, Ruben SM, Ni J, Feng P;
XX
DR WPI; 2002-281068/32.
XX
PT Novel nucleic acid molecules comprising a polynucleotide encoding human
PT tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides
PT useful for treating disease e.g. inflammatory and autoimmune disorders
PT -
XX
PS Claim 37; Page 348; 350pp; English.
XX
CC The invention relates to human tumour necrosis factor receptor (TNFR)-
CC 6alpha and 6beta protein and their corresponding nucleic acids. The
CC invention provides screening methods for identifying agonists and
CC antagonists of TNFR-6alpha and 6beta activity. The invention also
CC provides diagnostic and therapeutic methods for detecting and treating
CC immune system-related disorders. The method is useful for treating or
CC preventing an inflammatory disease or disorder selected from bowel
CC disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
CC disease or disorder selected from systemic lupus erythematosus,
CC arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
CC and autoimmune encephalitis, graft versus host disease (GVHD), and an
CC allergy or asthma. The present sequence is Mammalian synthetic TNFR-
CC 6alpha DNA.
XX
SQ Sequence 903 BP; 171 A; 253 C; 265 G; 214 T; 0 other;

Alignment Scores:

Pred. No.:	3.86e-77	Length:	903
Score:	1491.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-936-024-1 (1-271) x AAD33295 (1-903)

```
Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 GTGGCTGAAACACCTACATATCCATGGAGAGATGCTGAAACAGGAGAAAGGCTGGTGTGT 147

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GCTCAGTGTCCTCCTGGAACATTTGTGCAAAGGCCTTGTAGGCGCGATTCTCCTACGACG 207

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 TGTGGCCCTTGCCCTCCTAGGCACTATACACAGTTTTGGAACTATCTCGAGCGCTGTAGG 267

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 TATTGCAACGTGCTCTGTGGAGAAAGGGAAGAGGAAGCAAGGGCTTGTCATGCAACACAC 327

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACAGGGCATGTAGGTGTCGCACAGGCTTCTTTGCTCATGCTGGATTTTGTCTGGAACAC 387

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GCTTCTTGTCCTCCTGGTGCTGGAGTGATCGCTCCTGGTACACCCTCTCAGAACACCCAA 447

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 TGCCAGCCCTGTCCTCCTGGCACCTTCTCTGCATCTAGCTCCAGCTCTGAACAATGCCAA 507

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 CCTCACCGCAATTGTACAGCTCTGGGACTGGCTCTGAACGTGCCTGGTTCCTCCTCCCAT 567

Qy    161 AspThrLeuCysThrSerCysThrGlyProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GATACTCTGTGTACAAGCTGTACTGGCTTTCCTCTCTCTACCCGCGTGCCTGGCGCTGAA 627

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 GAGTGCGAACGCGCTGTGATCGACTTTGTGGCCTTCCAGGATATCTCTATCAAAAGGCTG 687

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 CAACGCCTGCTGCAAGCTCTGGAAGCTCCTGAGGGCTGGGGTCCCACACCAAGGGCTGGC 747

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 AGGGCTGCACTGCAACTGAAGCTTCGCAGGAGGCTCACTGAACTCCTGGGAGCTCAAGAT 807

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 GGAGCTCTGCTGGTGAGGCTGCTGCAAGCTCTGAGGGTGGCAAGGATGCCTGGACTGGAG 867

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          ||||||||||||||||||||||||||||||||
Db    868 CGCTCTGTGAGGGAACGCTTCCTGCCTGTGCAC 900
```

RESULT 12
AAF62705
ID AAF62705 standard; cDNA; 1055 BP.
XX
AC AAF62705;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human NTR3 nucleotide sequence.
XX
KW Human; NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;
KW antianaemic; immunosuppressive; antidiabetic; antiviral; antibacterial;
KW cytostatic; neuroprotective; antiinflammatory; anorectic; vasotropic;
KW antirheumatoid; antiarthritic; cerebroprotective; tuberculostatic;
KW gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;
KW infection; ss.
XX
OS Homo sapiens.
XX
PN WO200110908-A1.
XX
PD 15-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-US21287.
XX
PR 04-AUG-1999; 99US-0147297.
XX
PA (AMGE-) AMGEN INC.
XX
PI Hsu H;
XX
DR WPI; 2001-191521/19.
DR P-PSDB; AAB71754.
XX
PT New tumor necrosis factor receptor, NTR3, useful for treating cancers,
PT stroke, anemia, obesity, rheumatoid arthritis and transplantation
PT rejection -
XX
PS Claim 1; Page 128-129; 135pp; English.
XX
CC The present sequence encodes the tumour necrosis factor (TNF) receptor
CC polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful
CC for treating diseases such as acquired-immunodeficiency syndrome (AIDS),
CC anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,

```
CC   diabetes mellitus, disseminated intravascular coagulopathy, erythroid
CC   sick syndrome, haemorrhagic shock, hepatitis, insulin resistance,
CC   leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,
CC   obesity, rejection of transplanted organs, rheumatoid arthritis, septic
CC   shock syndrome, stroke, adult respiratory distress syndrome (ARDS),
CC   tuberculosis, and a number of viral diseases. The NTR3 polypeptide is
CC   useful for identifying or developing new (ant)agonists of NTR3. It may
CC   be used as an immunogen to which antibodies may be raised. NTR3 nucleic
CC   acid molecules may be useful as hybridisation probes in diagnostic assays
CC   to test, either qualitatively or quantitatively, for the presence of an
CC   NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid
CC   samples.
XX
SQ   Sequence 1055 BP; 160 A; 369 C; 340 G; 186 T; 0 other;

Alignment Scores:
Pred. No.:              4.54e-77      Length:        1055
Score:                  1491.00       Matches:       271
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     22            Gaps:          0

US-09-936-024-1 (1-271) x AAF62705 (1-1055)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 213

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 273

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 333

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 393

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 453

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 513

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 573

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 633

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 693

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 753

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 813

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 873

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 933

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db    934 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 966

RESULT 13
AAA53802
ID   AAA53802 standard; cDNA; 1066 BP.
XX
AC   AAA53802;
XX
DT   19-DEC-2000  (first entry)
XX
DE   M68 TNF receptor related protein coding sequence.
XX
KW   M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
KW   receptor; immune response; cell differentiation; ligand; cancer;
KW   bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
KW   Grave's disease; idiopathic myxodema; autoimmune diabetes;
KW   thrombotic thrombocytopenic purpura; multiple sclerosis;
KW   liver diseases; autoimmune gastritis; ulcerative colitis;
KW   glomerulonephritis; pulmonary fibrosis; heart failure;
KW   atherosclerosis; aplastic anaemia; myelodisplastic syndromes;
KW   osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
KW   myocardial infarction; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53..955
FT                   /*tag= a
FT                   /product= M68 polypeptide
XX
PN   WO200046247-A1.
XX
PD   10-AUG-2000.
XX
PF   04-FEB-2000; 2000WO-US03037.
XX
PR   05-FEB-1999;   99US-0118902.
PR   20-DEC-1999;   99US-0172754.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Bai C;
XX
DR   WPI; 2000-506066/45.
DR   P-PSDB; AAY97246.
XX
PT   Isolated human M68 nucleic acids and proteins which are part of the
PT   tumor necrosis factor receptor (TNFR) family, useful for identifying
PT   modulators that may be used to treat various diseases e.g. cancer,
PT   osteoporosis, Alzheimer's disease
XX
PS   Claim 21; Page 73-75; 80pp; English.
XX
CC   The M68 protein is a member of a family of proteins which have
CC   roles in immune responses, cell death, cell proliferation and
CC   stimulation of cell differentiation. M68 lacks a transmembrane domain
CC   and is a secreted factor suggesting that it functions as a natural
CC   inhibitor for its ligand. The altered expression pattern of M68 in a
CC   multitude of tissues suggests that M68 may play a role in cancer by
CC   binding to its ligand and blocking apoptotic cell death induced by
CC   such a ligand. This anti-apoptopic role of M68 suggests that
CC   modulators of M68 will be useful in treatment of apoptosis-related
CC   diseases such as various forms of cancer and various bone disorders.
CC   M68 nucleic acids and proteins are therefore useful for treating
CC   conditions involving atypical apoptosis and for identifying
CC   modulators of M68. Modulators of M68 are useful for treatment of
CC   cancer and other diseases associated with abnormal levels of
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```
CC   apoptosis including systemic lupus erythematosus, Hashimoto's
CC   thyroiditis, Grave's disease, idiopathic myxodema, autoimmune
CC   diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
CC   liver diseases, autoimmune gastritis, ulcerative colitis,
CC   glomerulonephritis, pulmonary fibrosis, heart failure,
CC   atherosclerosis, aplastic anaemia, myelodisplastic syndromes,
CC   osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
CC   myocardial infarction.
XX
SQ   Sequence 1066 BP; 178 A; 367 C; 335 G; 186 T; 0 other;

Alignment Scores:
Pred. No.:              4.59e-77        Length:         1066
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     21              Gaps:           0

US-09-936-024-1 (1-271) x AAA53802 (1-1066)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     140 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 199

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 259

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     260 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 319

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     320 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 379

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     380 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 439

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     440 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 499

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     500 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 559

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     560 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 619

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     620 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 679

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     680 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 739

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     740 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 799

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     800 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 859

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     860 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 919

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
           |||||||||||||||||||||||||||||||
Db     920 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 952

RESULT 14
AAV39085
ID   AAV39085 standard; cDNA; 1077 BP.
XX
AC   AAV39085;
XX
DT   26-OCT-1998  (first entry)
XX
DE   Human tumour necrosis factor receptor-6 alpha cDNA.
XX
KW   Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW   endothelial cells; keratinocytes; normal prostate; apoptosis;
KW   prostate tumour tissue; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             25..927
FT                   /*tag=  a
FT                   /product= "TNFR-6 alpha protein"
FT   sig_peptide     25..114
FT                   /*tag=  b
FT   mat_peptide     115..924
FT                   /*tag=  c
XX
PN   WO9830694-A2.
XX
PD   16-JUL-1998.
XX
PF   13-JAN-1998;   98WO-US00153.
XX
PR   14-JAN-1997;   97US-0035496.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ebner R,  Feng P,  Gentz RL,  Ni J,  Ruben SM,  Yu G;
XX
DR   WPI; 1998-399142/34.
DR   P-PSDB; AAW63622.
XX
PT   Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
PT   the diagnosis of immune system-related disorder(s)
XX
PS   Disclosure; Fig 1; 91pp; English.
XX
CC   The present sequence represents the human tumour necrosis factor
CC   receptor-6 alpha (TNFR-6 alpha) cDNA.  The invention also provides
CC   for the TNFR-6 beta cDNA (AAV39086).  TNFR-6 alpha and TNFR-6 beta are
CC   members of the tumour necrosis factor receptor (TNFR) family.  TNFRs
CC   are expressed in endothelial cells, keratinocytes, normal prostate and
CC   prostate tumour tissue.  For a number of disorders of these cells,
CC   particularly of the immune system, substantially altered (whether
CC   increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
CC   expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
CC   polypeptides, nucleic acids and antibodies are claimed to be useful in
CC   the diagnosis of such disorders.  Mutations of the TNFR-6 alpha and
CC   TNFR-6 beta genes can also be detected.  The TNFR polypeptides are
CC   also claimed to be useful for identifying ligands which may be useful
CC   in the treatment of apoptosis related disorders.
XX
SQ   Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

Alignment Scores:
Pred. No.:              4.64e-77        Length:         1077
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     19              Gaps:           0
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US-09-936-024-1 (1-271) x AAV39085 (1-1077)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 171

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 231

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 291

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 351

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 411

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 471

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 531

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 591

Qy     161 AspThrLeuCysThrSerCysThrGlyProProLeuSerThrArgValProGlyAlaGlu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 651

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     652 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 711

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 771

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     772 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 831

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 891

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
           ||||||||||||||||||||||||||||||||
Db     892 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 924
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RESULT 15
AAA37772
ID   AAA37772 standard; DNA; 1077 BP.
XX
AC   AAA37772;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Human tumour necrosis factor receptor-6 alpha coding sequence.
XX
KW   Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;
KW   ocular neovascularisation; solid tumour; malignancy; prostate cancer;
KW   breast cancer; colon cancer; diabetic retinopathy; microbial infection;
KW   pre-maturity macular degeneration; allergy; inflammation; tissue damage;
KW   thyroid associated opthalmopathy; cell damage; parasitic infection;
KW   bone disease; osteoporosis; atherosclerosis; cardiovascular disease;
KW   neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW   graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
KW   psoriasis; septic shock; ulcerative colitis; therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             25..927
FT                   /*tag=  a
FT                   /product= TNFR-6alpha
XX
PN   WO200052028-A1.
XX
PD   08-SEP-2000.
XX
PF   03-MAR-2000; 2000WO-US05686.
XX
PR   04-MAR-1999;   99US-0121774.
PR   12-MAR-1999;   99US-0124092.
PR   27-APR-1999;   99US-0131279.
PR   30-APR-1999;   99US-0131964.
PR   02-AUG-1999;   99US-0146371.
PR   01-DEC-1999;   99US-0168235.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Gentz RL,  Ni J,  Ebner R,  Yu G,  Ruben SM,  Feng P;
XX
DR   WPI; 2000-572174/53.
DR   P-PSDB; AAY90357.
XX
PT   Nucleic acids encoding human tumour necrosis factor receptor (TNFR)
PT   proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.
PT   Alzheimer's disease, osteoporosis and graft rejection -
XX
PS   Claim 2; Fig 1; 332pp; English.
XX
CC   This sequence encodes the human tumour necrosis factor receptor 6
CC   alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA
CC   and protein sequences can be used in the prevention, treatment and
CC   diagnosis of diseases associated with inappropriate TNFR expression. The
CC   nucleic acids, polypeptides, antibodies, agonists and antagonists against
CC   them may be used for the treatment of a range of conditions such as
CC   disorders associated with neovascularisation (especially ocular
CC   neovascularisation) (such as solid tumours and malignancies (e.g.
CC   prostate cancer, breast cancer and colon cancer), diabetic retinopathy
CC   and pre-maturity macular degeneration), allergies, inflammation,
CC   thyroid associated opthalmopathy tissue/cell damage, wounds, microbial
CC   and parasitic infections, bone disease (e.g. osteoporosis),
CC   atherosclerosis, pain, cardiovascular disease (e.g. stroke),
CC   neurodegenerative disorders (e.g. Alzheimer's disease), immune
CC   disorders (e.g. graft rejection), rheumatism, liver disease,
CC   autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative
CC   colitis.
XX
SQ   Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;
```

```
Alignment Scores:
Pred. No.:              4.64e-77        Length:         1077
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     21              Gaps:           0

US-09-936-024-1 (1-271) x AAA37772 (1-1077)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 171
```

```
Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 231

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 291

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 351

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 411

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 471

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 531

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 591

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 651

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     652 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 711

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 771

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     772 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 831

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 891

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
           ||||||||||||||||||||||||||||||||
Db     892 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 924
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Search completed: January 6, 2003, 11:31:11
Job time : 236 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:32 ; Search time 21 Seconds
(without alignments)
535.242 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1491	100.0	300	1	TR6B_HUMAN	O95407 homo sapien
2	440.5	29.5	401	1	T11B_HUMAN	O00300 homo sapien
3	425.5	28.5	401	1	T11B_RAT	O08727 rattus norv
4	424.5	28.5	401	1	T11B_MOUSE	O08712 mus musculu
5	340.5	22.8	461	1	TR1B_HUMAN	P20333 homo sapien
6	332.5	22.3	474	1	TR1B_MOUSE	P25119 mus musculu
7	299.5	20.1	435	1	TNR3_HUMAN	P36941 homo sapien
8	288.5	19.3	655	1	TR21_MOUSE	Q9epu5 mus musculu
9	287	19.2	655	1	TR21_HUMAN	O75509 homo sapien
10	265.5	17.8	415	1	TNR3_MOUSE	P50284 mus musculu
11	260	17.4	349	1	CRMB_VARV	P34015 variola vir
12	257.5	17.3	349	1	CRMB_CAMPS	Q8uya7 camelpox vi
13	254.5	17.1	351	1	CRMB_COWPX	O73559 cowpox viru
14	244	16.4	283	1	TR14_HUMAN	Q92956 homo sapien
15	235.5	15.8	616	1	TR11_HUMAN	Q9y6q6 homo sapien
16	234.5	15.7	325	1	VT2_SFVKA	P25943 shope fibro
17	220.5	14.8	625	1	TR11_MOUSE	O35305 mus musculu
18	215.5	14.5	277	1	TNR4_HUMAN	P43489 homo sapien
19	211.5	14.2	271	1	TNR4_RAT	P15725 rattus norv
20	211	14.2	277	1	TNR5_HUMAN	P25942 homo sapien
21	210.5	14.1	326	1	VT2_MYXVL	P29825 myxoma viru
22	203	13.6	289	1	TNR5_MOUSE	P27512 mus musculu
23	202	13.5	269	1	TNR5_BOVIN	Q28203 bos taurus
24	194.5	13.0	272	1	TNR4_MOUSE	P47741 mus musculu
25	185	12.4	256	1	TNR9_MOUSE	P20334 mus musculu
26	182	12.2	595	1	TNR8_HUMAN	P28908 homo sapien
27	174	11.7	255	1	TNR9_HUMAN	Q07011 homo sapien
28	171.5	11.5	416	1	TR16_CHICK	P18519 gallus gall
29	171	11.5	180	1	TR22_MOUSE	Q9er62 mus musculu
30	168	11.3	425	1	TR16_RAT	P07174 rattus norv
31	163	10.9	332	1	TNR6_PIG	O77736 sus scrofa
32	162	10.9	417	1	TR16_MOUSE	Q9z0w1 mus musculu
33	158	10.6	427	1	TR16_HUMAN	P08138 homo sapien
34	155.5	10.4	327	1	TNR6_MOUSE	P25446 mus musculu
35	155	10.4	323	1	TNR6_BOVIN	P51867 bos taurus
36	153	10.3	241	1	TR18_HUMAN	Q9y5u5 homo sapien
37	152.5	10.2	430	1	TRLT_MACFA	Q9n092 macaca fasc
38	151.5	10.2	430	1	TRLT_HUMAN	Q969z4 homo sapien
39	148.5	10.0	176	1	TR23_MOUSE	Q9er63 mus musculu
40	148	9.9	250	1	TNR7_MOUSE	P41272 mus musculu
41	147.5	9.9	5376	1	ZAN_MOUSE	O88799 mus musculu
42	145	9.7	335	1	TNR6_HUMAN	P25445 homo sapien
43	143.5	9.6	471	1	TR1A_BOVIN	O19131 bos taurus
44	142.5	9.6	260	1	TNR7_HUMAN	P26842 homo sapien
45	137.5	9.2	324	1	TNR6_RAT	Q63199 rattus norv

ALIGNMENTS

RESULT 1
TR6B_HUMAN
ID TR6B_HUMAN STANDARD; PRT; 300 AA.
AC O95407;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE receptor for Fas ligand) (Decoy receptor 3) (DcR3) (M68).
GN TNFRSF6B OR DCR3 OR TR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/DcR3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFS14/LIGHT
CC and TNFSF6/FasL. Protects against apoptosis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.

```
CC       Detected in adult stomach, spinal cord, lymph node, trachea,
CC       spleen, colon and lung. Highly expressed in several primary tumors
CC       from colon, stomach, rectum, esophagus and in SW480 colon
CC       carcinoma cells.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF104419; AAD03056.1; -.
DR   EMBL; AF134240; AAD29688.1; -.
DR   EMBL; AF217796; AAF35244.1; -.
DR   EMBL; AF217793; AAF33685.1; -.
DR   EMBL; AF217794; AAF33686.1; -.
DR   EMBL; AL121845; CAC03668.1; -.
DR   EMBL; BC017065; AAH17065.1; -.
DR   Genew; HGNC:11921; TNFRSF6B.
DR   MIM; 603361; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     29
FT   CHAIN       30    300       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 6B.
FT   REPEAT      31     70       TNFR-CYS 1.
FT   REPEAT      72    113       TNFR-CYS 2.
FT   REPEAT     115    150       TNFR-CYS 3.
FT   REPEAT     152    193       TNFR-CYS 4.
FT   DISULFID    49     62       BY SIMILARITY.
FT   DISULFID    52     70       BY SIMILARITY.
FT   DISULFID    73     88       BY SIMILARITY.
FT   DISULFID    91    105       BY SIMILARITY.
FT   DISULFID    95    113       BY SIMILARITY.
FT   DISULFID   115    126       BY SIMILARITY.
FT   DISULFID   132    150       BY SIMILARITY.
FT   DISULFID   153    168       BY SIMILARITY.
FT   DISULFID   174    193       BY SIMILARITY.
FT   CARBOHYD   173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   300 AA;  32679 MW;  F90AEE33718449AF CRC64;

  Query Match             100.0%;  Score 1491;  DB 1;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy      61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy     121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy     241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
           |||||||||||||||||||||||||||||||
Db     270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 2
T11B_HUMAN
ID   T11B_HUMAN     STANDARD;      PRT;   401 AA.
AC   O00300; O60236; Q9UHP4;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN   TNFRSF11B OR OPG OR OCIF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Suggs S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung cancer;
RX   MEDLINE=98151033; PubMed=9492069;
RA   Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA   Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA   Tsuda E., Morinaga T., Higashio K.;
RT   "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT   osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT   osteoclastogenesis in vitro.";
RL   Endocrinology 139:1329-1337(1998).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC   TISSUE=Placenta;
RX   MEDLINE=98351569; PubMed=9688283;
RA   Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT   "Cloning and characterization of the gene encoding human
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL   Eur. J. Biochem. 254:685-691(1998).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 22-36 AND 378-401.
RX   MEDLINE=98238645; PubMed=9571159;
RA   Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA   Morinaga T., Tsuda E., Higashio K.;
RT   "Characterization of monomeric and homodimeric forms of
RT   osteoclastogenesis inhibitory factor.";
RL   Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN   [6]
RP   SEQUENCE OF 22-393 FROM N.A.
RC   TISSUE=Placenta;
RA   He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT   "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL   Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN   [7]
RP   SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX   MEDLINE=97312536; PubMed=9168977;
RA   Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA   Morinaga T., Higashio K.;
RT   "Isolation of a novel cytokine from human fibroblasts that
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RT   specifically inhibits osteoclastogenesis.";
RL   Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN   [8]
RP   TRAIL BINDING.
RX   MEDLINE=98269100; PubMed=9603945;
RA   Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA   Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
RA   James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT   "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RL   J. Biol. Chem. 273:14363-14367(1998).
RN   [9]
RP   CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX   MEDLINE=98148058; PubMed=9478964;
RA   Yamaguchi K., Kinosaki M., Goto M., Kobayashi F., Tsuda E.,
RA   Morinaga T., Higashio K.;
RT   "Characterization of structural domains of human osteoclastogenesis
RT   inhibitory factor.";
RL   J. Biol. Chem. 273:5117-5123(1998).
RN   [10]
RP   REVIEW.
RX   MEDLINE=21395914; PubMed=11505389;
RA   Hofbauer L.C., Neubauer A., Heufelder A.E.;
RT   "Receptor activator of nuclear factor-kappaB ligand and
RT   osteoprotegerin: potential implications for the pathogenesis and
RT   treatment of malignant bone diseases.";
RL   Cancer 92:460-470(2001).
CC   -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC       its function in osteoclastogenesis. Inhibits the activation of
CC       osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC       homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC       play a role in preventing arterial calcification. May act as decoy
CC       receptor for TRAIL and protect against apoptosis. TRAIL binding
CC       blocks the inhibition of osteoclastogenesis.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC       liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC       lymph node, trachea, adrenal gland, testis, and bone marrow.
CC       Detected at very low levels in brain, placenta and skeletal
CC       muscle. Highly expressed in fetal kidney, liver and lung.
CC   -!- INDUCTION: Upregulated by increasing calcium-concentration in the
CC       medium and estrogens. Downregulated by glucocorticoids.
CC   -!- PTM: N-glycosylated. Contains sialic acid residues.
CC   -!- PTM: N-terminus may be blocked.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U94332; AAB53709.1; -.
DR   EMBL; AB002146; BAA25910.1; -.
DR   EMBL; AB008822; BAA32076.1; -.
DR   EMBL; AB008821; BAA32076.1; JOINED.
DR   EMBL; BC030155; AAH30155.1; -.
DR   EMBL; AF134187; AAF20168.1; -.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:11909; TNFRSF11B.
DR   MIM; 602643; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT   SIGNAL       1     21
FT   CHAIN       22    401       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 11B.
FT   REPEAT      24     62       TNFR-CYS 1.
FT   REPEAT      65    105       TNFR-CYS 2.
FT   REPEAT     107    142       TNFR-CYS 3.
FT   REPEAT     145    185       TNFR-CYS 4.
FT   DOMAIN     198    269       DEATH 1.
FT   DOMAIN     270    365       DEATH 2.
FT   SITE       400    400       INVOLVED IN DIMERIZATION.
FT   DISULFID    41     54       BY SIMILARITY.
FT   DISULFID    44     62       BY SIMILARITY.
FT   DISULFID    65     80       BY SIMILARITY.
FT   DISULFID    83     97       BY SIMILARITY.
FT   DISULFID    87    105       BY SIMILARITY.
FT   DISULFID   107    118       BY SIMILARITY.
FT   DISULFID   124    142       BY SIMILARITY.
FT   DISULFID   145    160       BY SIMILARITY.
FT   DISULFID   166    185       BY SIMILARITY.
FT   CARBOHYD    98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      3      3       K -> N.
FT                                /FTId=VAR_013439.
FT   MUTAGEN    400    400       C->S: ABOLISHES DIMERIZATION.
FT   MUTAGEN    400    401       MISSING: ABOLISHES DIMERIZATION.
FT   CONFLICT   263    263       D -> A (IN REF. 1).
SQ   SEQUENCE   401 AA;  46040 MW;  EDF448B67D86C71E CRC64;

  Query Match             29.5%;  Score 440.5;  DB 1;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 8.7e-28;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           |.|   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db      26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
             :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db     146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy     183 ERAVIDF 189
           | |   |
Db     203 EEAFFRF 209


RESULT 3
T11B_RAT
ID   T11B_RAT       STANDARD;      PRT;   401 AA.
AC   O08727;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin).
GN   TNFRSF11B OR OPG.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryonic intestine;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
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RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Suggs S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
CC   -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC       its function in osteoclastogenesis. Inhibits the activation of
CC       osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC       seems to depend on the local RANKL/OPG ratio. May also play a role
CC       in preventing arterial calcification. May act as decoy receptor
CC       for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC       inhibition of osteoclastogenesis (By similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- INDUCTION: Upregulated by osteopontin.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U94330; AAB53707.1; -.
DR   HSSP; P25942; 1CDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    401       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 11B.
FT   REPEAT       24     62       TNFR-CYS 1.
FT   REPEAT       65    105       TNFR-CYS 2.
FT   REPEAT      107    142       TNFR-CYS 3.
FT   REPEAT      145    185       TNFR-CYS 4.
FT   DOMAIN      198    269       DEATH 1.
FT   DOMAIN      270    365       DEATH 2.
FT   SITE        400    400       INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT   DISULFID     41     54       BY SIMILARITY.
FT   DISULFID     44     62       BY SIMILARITY.
FT   DISULFID     65     80       BY SIMILARITY.
FT   DISULFID     83     97       BY SIMILARITY.
FT   DISULFID     87    105       BY SIMILARITY.
FT   DISULFID    107    118       BY SIMILARITY.
FT   DISULFID    124    142       BY SIMILARITY.
FT   DISULFID    145    160       BY SIMILARITY.
FT   DISULFID    166    185       BY SIMILARITY.
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    178.   178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   401 AA;  46192 MW;  FEC6A31F1D4E573A CRC64;

  Query Match             28.5%;  Score 425.5;  DB 1;  Length 401;
  Best Local Similarity   39.5%;  Pred. No. 1.3e-26;
  Matches   81;  Conservative   33;  Mismatches   86;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||| :|:| :| |||:::: |     | | |||   ||  |:  : | ||:
Db      26 PKYLHYDPETGRQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDYSYTDSWHTSDECVYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |  | :    |||:| ||||| ||:  ||| :|| |: |
Db      86 VCKELQTVKQECNRTHNRVCECEEGRYLELEFCLKHRSCPPGLGVLQAGTPERNTVCKRC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |: | ||::||| |    |:::|| :   |:|   :|:  | :   |
Db     146 PDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNV---CSGNREATQNCGIDVTLC 202

Qy     183 ERAVIDFVAFQDISIKRLQRLLQAL 207
           | |   |     |    |  |: :|
Db     203 EEAFFRFAVPTKIIPNWLSVLVDSL 227


RESULT 4
T11B_MOUSE
ID   T11B_MOUSE     STANDARD;      PRT;   401 AA.
AC   O08712; O70202;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN   TNFRSF11B OR OPG OR OCIF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Kidney;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Suggs S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
RP   AND ARG-296.
RC   STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RX   MEDLINE=98382527; PubMed=9714833;
RA   Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA   Higashio K.;
RT   "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT   gene and its expression in embryogenesis.";
RL   Gene 215:339-343(1998).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=21060987; PubMed=10952716;
RA   Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
RA   Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
RA   Simonet W.S.;
RT   "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
RT   osteoclasts and prevents vascular calcification by blocking a process
RT   resembling osteoclastogenesis.";
RL   J. Exp. Med. 192:463-474(2000).
CC   -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC       its function in osteoclastogenesis. Inhibits the activation of
CC       osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC       homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC       play a role in preventing arterial calcification. May act as decoy
CC       receptor for TRAIL and protect against apoptosis. TRAIL binding
CC       blocks the inhibition of osteoclastogenesis.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
CC       intestines and calvaria. Highly expressed in decidua and placenta,
CC       and in embryo.
CC   -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
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CC       whereas expression decreases at day 11 and increases from day 15
CC       to 17. On day 15 found in developing bone primordia,
CC       brachiocephalic artery and ductus arteriosus, left main bronchus,
CC       abdominal aorta and midgut.
CC   -!- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
CC       1,25-dihdroxyvitamin D3 and parathyroid hormone.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U94331; AAB53708.1; -.
DR   EMBL; AB013898; BAA28269.1; -.
DR   EMBL; AB013903; BAA33388.1; -.
DR   EMBL; AB013899; BAA33388.1; JOINED.
DR   EMBL; AB013900; BAA33388.1; JOINED.
DR   EMBL; AB013901; BAA33388.1; JOINED.
DR   EMBL; AB013902; BAA33388.1; JOINED.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:109587; Tnfrsf11b.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    401       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 11B.
FT   REPEAT       24     62       TNFR-CYS 1.
FT   REPEAT       65    105       TNFR-CYS 2.
FT   REPEAT      107    142       TNFR-CYS 3.
FT   REPEAT      145    185       TNFR-CYS 4.
FT   DOMAIN      198    269       DEATH 1.
FT   DOMAIN      283    365       DEATH 2.
FT   SITE        400    400       INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT   DISULFID     41     54       BY SIMILARITY.
FT   DISULFID     44     62       BY SIMILARITY.
FT   DISULFID     65     80       BY SIMILARITY.
FT   DISULFID     83     97       BY SIMILARITY.
FT   DISULFID     87    105       BY SIMILARITY.
FT   DISULFID    107    118       BY SIMILARITY.
FT   DISULFID    124    142       BY SIMILARITY.
FT   DISULFID    145    160       BY SIMILARITY.
FT   DISULFID    166    185       BY SIMILARITY.
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     138    138       R -> P (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
FT   VARIANT     161    161       I -> R (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
FT   VARIANT     165    165       N -> D (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
FT   VARIANT     288    288       S -> A (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
FT   VARIANT     296    296       L -> R (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
SQ   SEQUENCE   401 AA;  45923 MW;  CAA6102D3B312470 CRC64;

  Query Match             28.5%;  Score 424.5;  DB 1;  Length 401;
  Best Local Similarity   39.0%;  Pred. No. 1.6e-26;

  Matches   80;  Conservative   32;  Mismatches   88;  Indels    5;  Gaps    2;

Qy       5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
           | |   | ||| :|:| :| |||:::: |     | | |||   ||  |:  : | ||:
Db      26 PKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSP 85

Qy      65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
           :| | :   : |: |||| | |  | :    |||:| |||||:||:  ||| :|| |: |
Db      86 VCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTVCKKC 145

Qy     125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
           | | ||  :||   |  | ||:  || |   |:::|| :   |:|   :|:  | :   |
Db     146 PDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNV---CSGNREATQKCGIDVTLC 202

Qy     183 ERAVIDFVAFQDISIKRLQRLLQAL 207
           | |   |     |   |  |: :|
Db     203 EEAFFRFAVPTKIIPNWLSVLVDSL 227


RESULT 5
TR1B_HUMAN
ID   TR1B_HUMAN     STANDARD;      PRT;   461 AA.
AC   P20333; Q16042;
DT   01-FEB-1991 (Rel. 17, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE   necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
DE   [Contains: Tumor necrosis factor binding protein 2 (TBPII)].
GN   TNFRSF1B OR TNFR2 OR TNFBR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90260639; PubMed=2160731;
RA   Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA   Dower S.K., Cosman D., Goodwin R.G.;
RT   "A receptor for tumor necrosis factor defines an unusual family of
RT   cellular and viral proteins.";
RL   Science 248:1019-1023(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91045991; PubMed=2172983;
RA   Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA   Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT   "A second tumor necrosis factor receptor gene product can shed a
RT   naturally occurring tumor necrosis factor inhibitor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96299745; PubMed=8661109;
RA   Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA   Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA   Brodeur G.M.;
RT   "Physical mapping and genomic structure of the human TNFR2 gene.";
RL   Genomics 35:94-100(1996).
RN   [4]
RP   SEQUENCE OF 37-461 FROM N.A.
RX   MEDLINE=91370690; PubMed=1966549;
RA   Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
RA   Brockhaus M., Lesslauer W.;
RT   "Two human TNF receptors have similar extracellular, but distinct
RT   intracellular, domain sequences.";
RL   Cytokine 2:231-237(1990).
RN   [5]
RP   SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=90349572; PubMed=2166946;
RA   Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA   Ringold G.M.;
RT   "Complementary DNA cloning of a receptor for tumor necrosis factor
RT   and demonstration of a shed form of the receptor.";
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RL   Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN   [6]
RP   SEQUENCE OF 27-31.
RX   MEDLINE=90110215; PubMed=2153136;
RA   Engelmann H., Novick D., Wallach D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross-reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [7]
RP   SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX   MEDLINE=91056048; PubMed=2173696;
RA   Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA   Brockhaus M.;
RT   "Purification and partial amino acid sequence analysis of two
RT   distinct tumor necrosis factor receptors from HL60 cells.";
RL   J. Biol. Chem. 265:20131-20138(1990).
RN   [8]
RP   CHARACTERIZATION.
RX   MEDLINE=93016040; PubMed=1328224;
RA   Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA   Lipari M.T., Goeddel D.V.;
RT   "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT   Characterization of ligand binding, internalization, and receptor
RT   phosphorylation.";
RL   J. Biol. Chem. 267:21172-21178(1992).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP   TRAF2.
RX   MEDLINE=99221490; PubMed=10206649;
RA   Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT   "Structural basis for self-association and receptor recognition of
RT   human TRAF2.";
RL   Nature 398:533-538(1999).
CC   -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC       approximately 5-fold lower affinity for homotrimeric
CC       TNFSF1/lymphotoxin-alpha.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC   -!- PTM: Phosphorylated; mainly on serine residues and with a very low
CC       level on threonine residues.
CC   -!- PTM: A soluble form (tumor necrosis factor binding protein 2) is
CC       produced from the membrane form by proteolytic processing.
CC   -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
CC       Wyeth-Ayerst). Used to treat moderate to servere rheumatoid
CC       arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC       portion of TNFR2 linked to an Immuglobulin Fc chain. It binds to
CC       TNF-alpha and blocks its interactions with receptors.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
CC   -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC       WWW="http://www.enbrelinfo.com/".
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M32315; AAA59929.1; -.
DR   EMBL; U52165; AAC50622.1; -.
DR   EMBL; U52156; AAC50622.1; JOINED.
DR   EMBL; U52157; AAC50622.1; JOINED.
DR   EMBL; U52158; AAC50622.1; JOINED.
DR   EMBL; U52159; AAC50622.1; JOINED.
DR   EMBL; U52160; AAC50622.1; JOINED.
DR   EMBL; U52161; AAC50622.1; JOINED.
DR   EMBL; U52162; AAC50622.1; JOINED.
DR   EMBL; U52163; AAC50622.1; JOINED.
DR   EMBL; U52164; AAC50622.1; JOINED.
DR   EMBL; M55994; AAA36755.1; -.
DR   EMBL; S63368; AAB19824.2; -.
DR   EMBL; M35857; AAA63262.1; -.
DR   PIR; A35356; A35356.
DR   PIR; A36007; A36007.
DR   PIR; A36475; A36475.
DR   PIR; B35010; B35010.
DR   PIR; A23666; A23666.
DR   PDB; 1CA9; 12-APR-99.
DR   Genew; HGNC:11917; TNFRSF1B.
DR   MIM; 191191; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Phosphorylation; Pharmaceutical; 3D-structure.
FT   SIGNAL       1    22
FT   CHAIN       23   461       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1B, MEMBRANE FORM.
FT   CHAIN       27     ?       TUMOR NECROSIS FACTOR BINDING PROTEIN 2.
FT   DOMAIN      23   257       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   258   287       POTENTIAL.
FT   DOMAIN     288   461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      39    76       TNFR-CYS 1.
FT   REPEAT      77   118       TNFR-CYS 2.
FT   REPEAT     119   162       TNFR-CYS 3.
FT   REPEAT     163   201       TNFR-CYS 4.
FT   DISULFID    40    53       BY SIMILARITY.
FT   DISULFID    54    67       BY SIMILARITY.
FT   DISULFID    57    75       BY SIMILARITY.
FT   DISULFID    78    93       BY SIMILARITY.
FT   DISULFID    96   110       BY SIMILARITY.
FT   DISULFID   100   118       BY SIMILARITY.
FT   DISULFID   120   126       BY SIMILARITY.
FT   DISULFID   134   143       BY SIMILARITY.
FT   DISULFID   137   161       BY SIMILARITY.
FT   DISULFID   164   179       BY SIMILARITY.
FT   CARBOHYD   171   171       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   193   193       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   141   141       R -> P (IN REF. 5).
FT   CONFLICT   196   196       M -> R (IN REF. 2 AND 5).
FT   CONFLICT   363   363       A -> T (IN REF. 5).
SQ   SEQUENCE   461 AA;  48291 MW;  603D0AE1CD69ACBF CRC64;

  Query Match           22.8%;  Score 340.5;  DB 1;  Length 461;
  Best Local Similarity 29.7%;  Pred. No. 7.6e-20;
  Matches   89;  Conservative   43;  Mismatches  115;  Indels   53;  Gaps   11;

Qy       1 VAETPTYPWRDAETGE------------RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRH 48
             || ||  |    | |             :: |::| ||   :  | : | | |  |
Db      27 VAFTPYAP----EPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDST 82

Qy      49 YTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAG------FCLEHAS 102
           ||| ||::  |  |   |   : | :||    || | || |::          |
Db      83 YTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRK 142

Qy     103 CPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDT 162
           | || ||  ||| : :  |:|| ||||| ::||:: |:||: |  :     :||::| |
Db     143 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVA----IPGNASMDA 198

Qy     163 LCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE-----GWGPTP 217
           :||| :  |  :  |||    : |           :  |   :   ||        ||:|
Db     199 VCTSTS--PTRSMAPGAVHLPQPV-------STRSQHTQPTPEPSTAPSTSFLLPMGPSP 249

Qy     218 RA----GRAALQLKLRRRLTELLGAQDGALLVRLLQAL---RVARMP-GLERSVRERFLP 269
           |    |  || : |   :| |     | |:: ::  :   :| : |  |:|  :   ||
Db     250 PAEGSTGDFALPVGLIVGVTAL-----GLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLP 304


RESULT 6
TR1B_MOUSE
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ID   TR1B_MOUSE     STANDARD;      PRT;   474 AA.
AC   P25119; P97893;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE   necrosis factor receptor 2) (TNF-R2) (p75).
GN   TNFRSF1B OR TNFR2 OR TNFR-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE OF 1-26 FROM N.A.
RC   STRAIN=NOD;
RA   Jacob C.O., Liu J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-22 FROM N.A.
RC   TISSUE=Liver;
RA   Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC       approximately 5-fold lower affinity for homotrimeric
CC       TNFSF1/lymphotoxin-alpha (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60469; AAA39752.1; -.
DR   EMBL; M59378; AAA40463.1; -.
DR   EMBL; U39488; AAA85021.1; -.
DR   EMBL; X87128; CAA60618.1; -.
DR   PIR; B38634; B38634.
DR   HSSP; P19438; 1NCF.
DR   MGD; MGI:1314883; Tnfrsf1b.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    474       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 1B.
FT   DOMAIN       23    258       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    259    288       POTENTIAL.
FT   DOMAIN      289    474       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       39     77       TNFR-CYS 1.
FT   REPEAT       78    119       TNFR-CYS 2.
FT   REPEAT      120    164       TNFR-CYS 3.
FT   REPEAT      165    203       TNFR-CYS 4.
FT   DISULFID     40     54       BY SIMILARITY.
FT   DISULFID     55     68       BY SIMILARITY.
FT   DISULFID     58     76       BY SIMILARITY.
FT   DISULFID     79     94       BY SIMILARITY.
FT   DISULFID     97    111       BY SIMILARITY.
FT   DISULFID    101    119       BY SIMILARITY.
FT   DISULFID    121    127       BY SIMILARITY.
FT   DISULFID    136    145       BY SIMILARITY.
FT   DISULFID    139    163       BY SIMILARITY.
FT   DISULFID    166    181       BY SIMILARITY.
FT   CARBOHYD     69     69       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   474 AA;  50319 MW;  462EAE398C4D6563 CRC64;

  Query Match             22.3%;  Score 332.5;  DB 1;  Length 474;
  Best Local Similarity   29.7%;  Pred. No. 3.4e-19;
  Matches   81;  Conservative   44;  Mismatches  109;  Indels   39;  Gaps    9;

Qy      17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
           :: ||:|||| :|:  | : | | | |    ||| ||    |  |:  |   : | |||
Db      52 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRAC 111

Qy      77 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
             || | |  | :      |:|    |:  : | || || :   |: |  |: | ||||
Db     112 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 171

Qy     130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
           | ::||:: |:||| |: |      :||::| | :|     : :  | :  |   |
Db     172 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 227

Qy     186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 240
            :|    |:    :  :| :|      | ||       |  :| : |   :| |
Db     228 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 272

Qy     241 GALLVRLLQAL----RVARMPGLERSVRERFLP 269
           | |:: |:  :    |  :   |:|  :   :|
Db     273 GLLMLGLVNCIILVQRKKKPSCLQRDAKVPHVP 305


RESULT 7
TNR3_HUMAN
ID   TNR3_HUMAN     STANDARD;      PRT;   435 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 3 precursor
DE   (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE   protein) (Tumor necrosis factor C receptor).
GN   LTBR OR TNFRSF3 OR TNFCR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93252381; PubMed=8486360;
RA   Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   FUNCTION.
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RX   MEDLINE=94225209; PubMed=8171323;
RA   Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA   Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT   "A lymphotoxin-beta-specific receptor.";
RL   Science 264:707-710(1994).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=99223511; PubMed=10207006;
RA   Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT   "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RT   death in HeLa cells.";
RL   J. Biol. Chem. 274:11868-11873(1999).
RN   [5]
RP   FUNCTION.
RX   MEDLINE=20261554; PubMed=10799510;
RA   Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA   Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT   "The lymphotoxin-beta receptor is necessary and sufficient for
RT   LIGHT-mediated apoptosis of tumor cells.";
RL   J. Biol. Chem. 275:14307-14315(2000).
CC   -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC       LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC       and TRAF5. May play a role in the development of lymphoid organs.
CC   -!- SUBUNIT: Self-associates.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L04270; AAA36757.1; -.
DR   EMBL; BC026262; AAH26262.1; -.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:6718; LTBR.
DR   MIM; 600979; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     30       POTENTIAL.
FT   CHAIN       31    435       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 3.
FT   DOMAIN      31    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   228    248       POTENTIAL.
FT   DOMAIN     249    435       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      42     81       TNFR-CYS 1.
FT   REPEAT      82    124       TNFR-CYS 2.
FT   REPEAT     125    168       TNFR-CYS 3.
FT   REPEAT     169    211       TNFR-CYS 4.
FT   DISULFID    43     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     80       BY SIMILARITY.
FT   DISULFID    83     98       BY SIMILARITY.
FT   DISULFID   101    116       BY SIMILARITY.
FT   DISULFID   104    124       BY SIMILARITY.
FT   DISULFID   126    132       BY SIMILARITY.
FT   DISULFID   139    148       BY SIMILARITY.
FT   DISULFID   142    167       BY SIMILARITY.
FT   DISULFID   170    185       BY SIMILARITY.
FT   CARBOHYD    40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   435 AA;  46709 MW;  624626E6022F656F CRC64;

  Query Match           20.1%;  Score 299.5;  DB 1;  Length 435;
  Best Local Similarity 32.0%;  Pred. No. 1.2e-16;

  Matches   74;  Conservative   27;  Mismatches  101;  Indels   29;  Gaps   9;

Qy      13 ETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGER 69
           |   |: |::||||||:|   | |   | |: |    | : ||||   : || |: : |
Db      52 EPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG-- 109

Qy      70 EEEARACHATHNRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQ 122
           ||   | :    |||: | |  | : ||  |    : ||||   :       | | |
Db     110 LEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCV 168

Qy     123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEEC 182
           ||  | |  :|| | :|||| |   ||    ||::  || | :    ||   : |
Db     169 PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE-PLPPEMSGTMLM 227

Qy     183 ERAVIDFVAFQDIS------------IKRLQRLLQALEAPEGWGPTPRAG 220
             ::    |  ::              ::|  ||:    |:| || | ||
Db     228 LAVLLPLAFFLLLATVFSCIWKSHPSLCRKLGSLLK--RRPQGEGPNPVAG 276


RESULT 8
TR21_MOUSE
ID   TR21_MOUSE     STANDARD;      PRT;   655 AA.
AC   Q9EPU5; Q91XH9; Q91W77;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE   related death receptor-6) (Death receptor 6).
GN   TNFRSF21 OR DR6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Kidney;
RA   Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA   Minami M.;
RT   "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT   (DR6).";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Kidney;
RA   Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RT   "Murine DR6: murine TNFR-related death receptor-6.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   FUNCTION.
RX   MEDLINE=21571606; PubMed=11714751;
RA   Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT   "Impaired c-Jun amino terminal kinase activity and T cell
RT   differentiation in death receptor 6-deficient mice.";
RL   J. Exp. Med. 194:1441-1448(2001).
CC   -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
CC       similarity). May activate JNK and be involved in T-cell
CC       differentiation.
CC   -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC       May be involved in T-cell differentiation.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
CC       thymus, testis, prostate, ovary, small intestine, colon, brain,
CC       lung and kidney, and in fetal brain, liver and lung. Detected at
CC       lower levels in adult peripheral blood leukocytes, lung, and in
CC       fetal muscle, heart, kidney, small intestine and skin. Detected in
CC       T-cells, B-cells and monocytes. In T-cells expression is highest
CC       in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF322069; AAG38115.1; -.
DR   EMBL; AY043489; AAK74193.1; -.
DR   EMBL; BC016420; AAH16420.1; -.
DR   HSSP; O14763; 1D0G.
DR   MGD; MGI:2151075; Tnfrsf21.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     41       POTENTIAL.
FT   CHAIN       42    655       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 21.
FT   DOMAIN      42    349       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   350    370       POTENTIAL.
FT   DOMAIN     371    655       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     415    498       DEATH.
FT   REPEAT      50     88       TNFR-CYS 1.
FT   REPEAT      90    131       TNFR-CYS 2.
FT   REPEAT     133    167       TNFR-CYS 3.
FT   REPEAT     170    211       TNFR-CYS 4.
FT   DISULFID    67     80       BY SIMILARITY.
FT   DISULFID    70     88       BY SIMILARITY.
FT   DISULFID    91    106       BY SIMILARITY.
FT   DISULFID   109    123       BY SIMILARITY.
FT   DISULFID   113    131       BY SIMILARITY.
FT   DISULFID   133    144       BY SIMILARITY.
FT   DISULFID   150    168       BY SIMILARITY.
FT   DISULFID   171    186       BY SIMILARITY.
FT   DISULFID   192    211       BY SIMILARITY.
FT   CARBOHYD    82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   252    252       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   257    257       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   278    278       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   352    352       W -> L (IN REF. 1).
FT   CONFLICT   523    523       M -> I (IN REF. 3).
SQ   SEQUENCE   655 AA;  71982 MW;  5EC7C51C7C99EFF7 CRC64;

  Query Match             19.3%;  Score 288.5;  DB 1;  Length 655;
  Best Local Similarity   29.7%;  Pred. No. 1.4e-15;
  Matches   69;  Conservative   32;  Mismatches  116;  Indels   15;  Gaps    3;

Qy       6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 65
           ||   |  ||: | | :|| ||:|   |   |   |  ||   :|:  | :|||  |:
Db      53 TYRHVDRTTGQVLTCDKCPAGTYVSEHCTNMSLRVCSSCPAGTFTRHENGIERCHDCSQP 112

Qy      66 CGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCP 125
           |     |   | |  :| | |  | :   | |  |  || | ||    || ::: :|: |
Db     113 CPWPMIERLPCAALTDRECICPPGMYQSNGTCAPHTVCPVGWGVRKKGTENEDVRCKQCA 172

Qy     126 PGTPSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPL---STRVPGAEEC 182
            ||||   ||  :|: | :|    | :  ||:   | :|    |  |   ||  | :
Db     173 RGTFSDVPSSVMKCKAHTDCLGQNLEVVKPGTKETDNVC----GMRLFFSSTNPPSSGTV 228

Qy     183 ERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTE 234
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           :  : :   |:     :        |:|   |     |::: |:   : |
Db    229 TFSHPEHMESHDVPSSTYE--------PQGMNSTDSNSTASVRTKVPSGIEE 272


RESULT 9
TR21_HUMAN
ID   TR21_HUMAN     STANDARD;      PRT;   655 AA.
AC   O75509; Q96D86;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE   related death receptor-6) (Death receptor 6).
GN   TNFRSF21 OR DR6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98378343; PubMed=9714541;
RA   Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C.,
RA   Aggarwal B.B., Ni J., Dixit V.M.;
RT   "Identification and functional characterization of DR6, a novel death
RT   domain-containing TNF receptor.";
RL   FEBS Lett. 431:351-356(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Parker A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, and Colon;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC   -!- SUBUNIT: Associates with TRADD.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta,
CC       pancreas, lymph node, thymus and prostate. Detected at lower
CC       levels in lung, skeletal muscle, kidney, testis, uterus, small
CC       intestine, colon, spleen, bone marrow and fetal liver. Very low
CC       levels were found in adult liver and peripheral blood leukocytes.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF068868; AAC34583.1; -.
DR   EMBL; AL096801; CAB75692.1; -.
DR   EMBL; BC017730; AAH17730.1; -.
DR   EMBL; BC010241; AAH10241.1; ALT_INIT.
DR   Genew; HGNC:13469; TNFRSF21.
DR   MIM; 605732; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
```

```
FT   SIGNAL        1     41       POTENTIAL.
FT   CHAIN        42    655       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 21.
FT   DOMAIN       42    349       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    350    370       POTENTIAL.
FT   DOMAIN      371    655       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      415    498       DEATH.
FT   REPEAT       50     88       TNFR-CYS 1.
FT   REPEAT       90    131       TNFR-CYS 2.
FT   REPEAT      133    167       TNFR-CYS 3.
FT   REPEAT      170    211       TNFR-CYS 4.
FT   DISULFID     67     80       BY SIMILARITY.
FT   DISULFID     70     88       BY SIMILARITY.
FT   DISULFID     91    106       BY SIMILARITY.
FT   DISULFID    109    123       BY SIMILARITY.
FT   DISULFID    113    131       BY SIMILARITY.
FT   DISULFID    133    144       BY SIMILARITY.
FT   DISULFID    150    168       BY SIMILARITY.
FT   DISULFID    171    186       BY SIMILARITY.
FT   DISULFID    192    211       BY SIMILARITY.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    252    252       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    257    257       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    278    278       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   655 AA;  71844 MW;  48939391C4852A33 CRC64;
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Query Match 19.2%; Score 287; DB 1; Length 655;
Best Local Similarity 34.3%; Pred. No. 1.8e-15;
Matches 58; Conservative 23; Mismatches 88; Indels 0; Gaps 0;

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Qy       6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 65
Db      53 TYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQP 112

Qy      66 CGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCP 125
Db     113 CPWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCA 172

Qy     126 PGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLST 174
Db     173 RGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSST 221
```

```
RESULT 10
TNR3_MOUSE
ID   TNR3_MOUSE     STANDARD;      PRT;   415 AA.
AC   P50284;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 3 precursor
DE   (Lymphotoxin-beta receptor).
GN   LTBR OR TNFRSF3 OR TNFCR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CVB; TISSUE=Lung;
RX   MEDLINE=96072804; PubMed=7594541;
RA   Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA   Browning J.L., Ware C.F.;
RT   "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT   and expression.";
RL   J. Immunol. 155:5280-5288(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96163885; PubMed=8586432;
RA   Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA   Honjo T.;
RT   "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT   sequence trap and chromosomal mapping.";
RL   Genomics 30:312-319(1995).
CC   -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC       LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC       and TRAF5. May play a role in the development of lymphoid organs
CC       (By similarity).
CC   -!- SUBUNIT: Self-associates (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U29173; AAA68964.1; -.
DR   EMBL; L38423; AAB00846.1; -.
DR   EMBL; U30798; AAA81334.1; -.
DR   HSSP; O14763; 1D0G.
DR   MGD; MGI:104875; Ltbr.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    415       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 3.
FT   DOMAIN       31    223       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      245    415       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       42     81       TNFR-CYS 1.
FT   REPEAT       82    124       TNFR-CYS 2.
FT   REPEAT      125    170       TNFR-CYS 3.
FT   REPEAT      171    213       TNFR-CYS 4.
FT   DISULFID     43     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     80       BY SIMILARITY.
FT   DISULFID     83     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    132       BY SIMILARITY.
FT   DISULFID    139    150       BY SIMILARITY.
FT   DISULFID    142    169       BY SIMILARITY.
FT   DISULFID    172    187       BY SIMILARITY.
FT   CARBOHYD     40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   415 AA;  44956 MW;  29B326A566AEF661 CRC64;
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Query Match 17.8%; Score 265.5; DB 1; Length 415;
Best Local Similarity 30.9%; Pred. No. 5.6e-14;
Matches 72; Conservative 24; Mismatches 88; Indels 49; Gaps 10;

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Qy      20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGEREEEARAC 76
Db      59 CSRCPPGEFVFAVCSRSQDTVCKTCPHNSYNEHWNHLSTCQLCRPCDIVLG--FEEVAPC 116

Qy      77 HATHNRACRCRTGFFAHAGFCL----EHASCPPGAGVIA-PGTPSQNT--------QCQP 123
Db     117 TSDRKAECRCQPGM-----SCVYLDNECVHCEEERLVLCQPGTEAEVTDEIMDTDVNCVP 171

Qy     124 CPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECE 183
Db     172 CKPGHFQNTSSPRARCQPHTRCEIQGLVEAAPGTSYSDTICK-------NPPEPGAMLLL 224

Qy     184 RAVIDFVAF-------------QDISIKRLQRLLQALEAPEGWG----PTPRA 219
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```
Db    225 AILLSLVLFLLFTTVLACAWMRHPSLCRKLGTLLK--RHPEGEESPPCPAPRA 275


RESULT 11
CRMB_VARV
ID   CRMB_VARV      STANDARD;      PRT;   349 AA.
AC   P34015; Q89098; Q85407; Q89118;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   CRMB OR G2R OR G4R.
OS   Variola virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10255;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=India-1967 / Isolate Ind3;
RX   MEDLINE=93202281; PubMed=8384129;
RA   Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT   "Genes of variola and vaccinia viruses necessary to overcome the host
RT   protective mechanisms.";
RL   FEBS Lett. 319:80-83(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bangladesh-1975;
RX   MEDLINE=94088747; PubMed=8264798;
RA   Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
RA   Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA   Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA   Venter C.J.;
RT   "Potential virulence determinants in terminal regions of variola
RT   smallpox virus genome.";
RL   Nature 366:748-751(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966, and Somalia-1977;
RA   Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA   Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966;
RX   MEDLINE=20107289; PubMed=10639322;
RA   Shchelkunov S.N., Totmenin A.V., Loparev V.N., Safronov P.F.,
RA   Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Massung R.F.,
RA   Esposito J.J.;
RT   "Alastrim smallpox variola minor virus genome DNA sequences.";
RL   Virology 266:361-386(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X69198; CAA49137.1; -.
DR   EMBL; X67117; CAA47540.1; -.
DR   EMBL; L22579; AAA60933.1; -.
DR   EMBL; U18339; AAA69407.1; -.
DR   EMBL; U18341; AAA69467.1; -.
DR   EMBL; Y16780; CAB54798.1; -.
DR   EMBL; U88146; AAB94371.1; -.
DR   EMBL; U88148; AAB94373.1; -.
DR   EMBL; U88149; AAB94374.1; -.
DR   EMBL; U88152; AAB94377.1; -.
DR   PIR; D36858; D36858.
DR   PIR; S35987; S35987.
DR   PIR; S46888; S46888.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1    22       POTENTIAL.
FT   CHAIN       23   349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT      31    66       TNFR-CYS 1.
FT   REPEAT      67   108       TNFR-CYS 2.
FT   DISULFID    32    43       BY SIMILARITY.
FT   DISULFID    44    57       BY SIMILARITY.
FT   DISULFID    47    65       BY SIMILARITY.
FT   DISULFID    68    83       BY SIMILARITY.
FT   DISULFID    86   100       BY SIMILARITY.
FT   DISULFID    90   108       BY SIMILARITY.
FT   CARBOHYD   101   101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   173   173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   189   189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   215   215       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   248   248       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     17    17       MISSING (IN STRAINS BANGLADESH-1975 AND
FT                              CHIMP 9-4).
FT   VARIANT    160   160       H -> Y (IN STRAINS BUTLER-1952, GARCIA-
FT                              1966 AND SOMALIA-1977).
FT   VARIANT    165   165       A -> T (IN STRAINS BUTLER-1952 AND
FT                              GARCIA-1966).
FT   VARIANT    182   182       E -> K (IN STRAIN SOMALIA-1977).
FT   VARIANT    274   274       A -> E (IN STRAIN SOMALIA-1977).
FT   VARIANT    335   335       N -> D (IN STRAINS BUTLER-1952 AND
FT                              GARCIA-1966).
FT   VARIANT    339   339       P -> L (IN STRAINS BUTLER-1952 AND
FT                              GARCIA-1966).
SQ   SEQUENCE   349 AA;  38189 MW;  D45D40B5C6E780EF CRC64;

  Query Match             17.4%;  Score 260;  DB 1;  Length 349;
  Best Local Similarity   32.2%;  Pred. No. 1.3e-13;
  Matches   59;  Conservative   26;  Mismatches   90;  Indels    8;  Gaps    3;

Qy       5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN 63
           |    :| |     | |  |||||:  | |   : | | ||    :|   |:|  |  ||
Db      28 PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 87

Qy      64 VLCGEREEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQ 117
             |   : | |:|: |||| | |  |::      :    |:    |  | || : |
Db      88 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 146

Qy     118 NTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
           :  | ||  ||:| : ||:::|:|  | |   : : :     :|| ||  |   ||  :
Db     147 DVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL 206

Qy     178 GAE 180
           :|
Db     207 TSE 209


RESULT 12
CRMB_CAMPS
ID   CRMB_CAMPS     STANDARD;      PRT;   349 AA.
```

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AC   Q8UYA7;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).
OS   Camelpox virus (strain CMS), and
OS   Camelpox virus (strain M-96).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=203172, 203173;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CMS;
RX   PubMed=11907336;
RA   Gubser C., Smith G.L.;
RT   "The sequence of camelpox virus shows it is most closely related to
RT   variola virus, the cause of smallpox.";
RL   J. Gen. Virol. 83:855-872(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=M-96;
RA   Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
RA   Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
RT   "The genome of camelpox virus.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY009089; AAG37456.1; -.
DR   EMBL; AY009089; AAG37718.1; -.
DR   EMBL; AF438165; AAL73920.1; -.
DR   EMBL; AF438165; AAL73917.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT       31     65       TNFR-CYS 1.
FT   REPEAT       67    108       TNFR-CYS 2.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     65       BY SIMILARITY.
FT   DISULFID     68     83       BY SIMILARITY.
FT   DISULFID     86    100       BY SIMILARITY.
FT   DISULFID     90    108       BY SIMILARITY.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   349 AA;  38064 MW;  EA412AF991E087F3 CRC64;

  Query Match             17.3%;  Score 257.5;  DB 1;  Length 349;
  Best Local Similarity   32.0%;  Pred. No. 2e-13;
  Matches   54;  Conservative   28;  Mismatches   80;  Indels    7;  Gaps    2;

Qy      18 LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACH 77
           | |  |||||:  | |   : | | ||    :|   |:|  |  ||  |   : | |:|:
Db      42 LCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCNGRCDSNQVETRSCN 101

Qy      78 ATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA 131
           ||||| | |  |::       :    |:    |  | || :  | : :  | ||  ||:|
Db     102 TTHNRICECSPGYYCILKGSSGCKACVSQTKCGIGYGV-SGHTSAGDVICSPCGLGTYSR 160

Qy     132 SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           : ||:::|:|  : |   : : :    :|| ||  |   :|  :  :|
Db     161 TVSSADKCEPVPSNTFNYIDVEINLYPVNDTSCTRTTTTGISESISTSE 209


RESULT 13
CRMB_COWPX
ID   CRMB_COWPX     STANDARD;      PRT;   351 AA.
AC   O73559;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR D2L) AND (CRMB2 OR H4R).
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GRI-90 / Grishak;
RX   MEDLINE=98229462; PubMed=9568042;
RA   Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA   Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT   "The genomic sequence analysis of the left and right species-specific
RT   terminal region of a cowpox virus strain reveals unique sequences and
RT   a cluster of intact ORFs for immunomodulatory and host range
RT   proteins.";
RL   Virology 243:432-460(1998).
RN   [2]
RP   FUNCTION.
RC   STRAIN=Brighton red;
RX   PubMed=8091665;
RA   Hu F.Q., Smith C.A., Pickup D.J.;
RT   "Cowpox virus contains two copies of an early gene encoding a soluble
RT   secreted form of the type II TNF receptor.";
RL   Virology 204:343-356(1994).
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11842; CAA72578.1; -.
DR   EMBL; Y15035; CAA75306.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    351       SOLUBLE TNF RECEPTOR II.
FT   REPEAT       31     67       TNFR-CYS 1.
FT   REPEAT       69    110       TNFR-CYS 2.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     67       BY SIMILARITY.
FT   DISULFID     70     85       BY SIMILARITY.
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FT   DISULFID     88    102       BY SIMILARITY.
FT   DISULFID     92    110       BY SIMILARITY.
FT   CARBOHYD    103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    250    250       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   351 AA;  38253 MW;  57CAE73EF4E5D7C7 CRC64;

  Query Match             17.1%;  Score 254.5;  DB 1;  Length 351;
  Best Local Similarity   32.2%;  Pred. No. 3.4e-13;
  Matches   55;  Conservative   29;  Mismatches   78;  Indels    9;  Gaps    3;

Qy      18 LVCAQCPPGTFVQRPC--RRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARA 75
           | |  |||||:  | |  : :: | | ||    :|   |:|  |  ||  |   : | |:
Db      42 LCCLSCPPGTYASRLCDSKTNTNTQCTPCGSGTFTSRNNHLPACLSCNGRCDSNQVETRS 101

Qy      76 CHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
           |: |||| | |  |::      :    |:    |  | || :  | : :  | ||  ||:
Db     102 CNTTHNRICECAPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSTGDVVCSPCGLGTY 160

Qy     130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           | : ||:::|:|  : |   : : :     :|| ||  |   ||  :  :|
Db     161 SHTVSSADKCEPVPSNTFNYIDVEINLYPVNDTSCTRTTTGLSESISTSE 211


RESULT 14
TR14_HUMAN
ID   TR14_HUMAN     STANDARD;      PRT;   283 AA.
AC   Q92956; Q9UM65; Q96J31; Q8WXR1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 14 precursor
DE   (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
DE   (TR2).
GN   TNFRSF14 OR HVEM OR HVEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cervical adenocarcinoma;
RX   MEDLINE=97053782; PubMed=8898196;
RA   Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT   "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT   the TNF/NGF receptor family.";
RL   Cell 87:427-436(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97306336; PubMed=9162061;
RA   Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA   Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA   Porter T.G., Truneh A., Young P.R.;
RT   "A newly identified member of the tumor necrosis factor receptor
RT   superfamily with a wide tissue distribution and involvement in
RT   lymphocyte activation.";
RL   J. Biol. Chem. 272:14272-14276(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Zhang W., Wan T., Cao X.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
RX   MEDLINE=21629477; PubMed=11756979;
RA   Struyf F., Posavad C.M., Keyaerts E., Van Ranst M., Corey L.,
RA   Spear P.G.;
RT   "Search for polymorphisms in the genes for herpesvirus entry mediator,
RT   Nectin-1, and Nectin-2 in immune seronegative individuals.";
RL   J. Infect. Dis. 185:36-44(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
RX   MEDLINE=21403268; PubMed=11511370;
RA   Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
RA   Eisenberg R.J., Wiley D.C.;
RT   "Herpes simplex virus glycoprotein D bound to the human receptor
RT   HveA.";
RL   Mol. Cell 8:169-179(2001).
CC   -!- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
CC       an important role in HSV pathogenesis because it enhanced the
CC       entry of several wildtype HSV strains of both serotypes into CHO
CC       cells, and mediated HSV entry into activated human T cells.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC       IN LUNG, SPLEEN, AND THYMUS.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U70321; AAB58354.1; -.
DR   EMBL; U81232; AAD00505.1; -.
DR   EMBL; AF153978; AAF75588.1; -.
DR   EMBL; AF373877; AAL47717.1; -.
DR   EMBL; AF373878; AAL47718.1; -.
DR   EMBL; BC002794; AAH02794.1; -.
DR   PDB; 1JMA; 26-SEP-01.
DR   Genew; HGNC:11912; TNFRSF14.
DR   MIM; 602746; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW   3D-structure.
FT   SIGNAL       1     38       POTENTIAL.
FT   CHAIN       39    283       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 14.
FT   DOMAIN      39    202       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   203    223       POTENTIAL.
FT   DOMAIN     224    283       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      42     75       TNFR-CYS 1.
FT   REPEAT      78    119       TNFR-CYS 2.
FT   REPEAT     121    162       TNFR-CYS 3.
FT   DISULFID    42     53
FT   DISULFID    54     67
FT   DISULFID    57     75
FT   DISULFID    78     93
FT   DISULFID    96    111
FT   DISULFID    99    119
FT   DISULFID   121    138
FT   DISULFID   127    135
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     17     17       K -> R.
FT                               /FTId=VAR_013007.
FT   VARIANT    241    241       V -> I.
FT                               /FTId=VAR_013440.
SQ   SEQUENCE   283 AA;  30392 MW;  46CE13C2C70242C1 CRC64;

  Query Match             16.4%;  Score 244;  DB 1;  Length 283;
  Best Local Similarity   37.3%;  Pred. No. 1.8e-12;
  Matches   56;  Conservative   14;  Mismatches   68;  Indels   12;  Gaps    4;
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```
Qy      20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLER---CRYCNVLCGEREEEARAC 76
           | :| ||  |: |   : | | ||||  |    | | :   |: |:   | |   :| |
Db      54 CPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLR--ASRNC 111

Qy      77 HATHNRACRCRTGFFA------HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFS 130
             | |  | |  | |       |   |  :|:  ||  |   || ||:| || |||||||
Db     112 SRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS 171

Qy     131 ASSSSSEQCQPHRNCTALGLALNVPGSSSH 160
           : : |:||    |: |       ||||
Db     172 -PNGTLEECQHQTKCSWLVTKAGAGTSSSH 200


RESULT 15
TR11_HUMAN
ID   TR11_HUMAN     STANDARD;      PRT;   616 AA.
AC   Q9Y6Q6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11A precursor
DE   (Receptor activator of NF-KB) (Osteoclast differentiation factor
DE   receptor) (ODFR).
GN   TNFRSF11A OR RANK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dendritic cell;
RX   MEDLINE=98032977; PubMed=9367155;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=99097247; PubMed=9878548;
RA   Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA   Morinaga T., Higashio K.;
RT   "RANK is the essential signaling receptor for osteoclast
RT   differentiation factor in osteoclastogenesis.";
RL   Biochem. Biophys. Res. Commun. 253:395-400(1998).
RN   [3]
RP   VARIANT FEO 16-L--L-21 DUPL, VARIANT PDB2 13-A--L-21 DUPL, AND VARIANT
RP   V-192.
RX   MEDLINE=20082806; PubMed=10615125;
RA   Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
RA   Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
RA   Anderson D.M.;
RT   "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RT   familial expansile osteolysis.";
RL   Nat. Genet. 24:45-48(2000).
CC   -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for
CC       RANKL-mediated osteoclastogenesis. Involved in the regulation of
CC       interactions between T-cells and dendritic cells.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC       SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
CC       GLAND.
CC   -!- DISEASE: DEFECTS IN TNFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE
CC       OSTEOLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER
CC       CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE
CC       OSTEOLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING EARLY
CC       ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS AND
CC       LOSS OF DENTITION.
CC   -!- DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET
CC       DISEASE OF BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT
CC       IS A BONE REMODELLING DISORDER WITH CLINICAL SIMILARITIES TO FEO.
CC       UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE
CC       AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF018253; AAB86809.1; -.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:11908; TNFRSF11A.
DR   MIM; 603499; -.
DR   MIM; 174810; -.
DR   MIM; 602080; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW   Disease mutation.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    616       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 11A.
FT   DOMAIN       30    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    233       POTENTIAL.
FT   DOMAIN      234    616       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       34     68       TNFR-CYS 1.
FT   REPEAT       71    112       TNFR-CYS 2.
FT   REPEAT      114    151       TNFR-CYS 3.
FT   REPEAT      154    194       TNFR-CYS 4.
FT   DISULFID     34     46       BY SIMILARITY.
FT   DISULFID     47     60       BY SIMILARITY.
FT   DISULFID     50     68       BY SIMILARITY.
FT   DISULFID     71     86       BY SIMILARITY.
FT   DISULFID     92    112       BY SIMILARITY.
FT   DISULFID    114    127       BY SIMILARITY.
FT   DISULFID    133    151       BY SIMILARITY.
FT   CARBOHYD    105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      21     21       L -> LALLLLCALL (IN PDB2).
FT                                 /FTId=VAR_011516.
FT   VARIANT      21     21       L -> LLLCALL (IN FEO).
FT                                 /FTId=VAR_011517.
FT   VARIANT     192    192       A -> V.
FT                                 /FTId=VAR_011518.
SQ   SEQUENCE   616 AA;  66033 MW;  E3DE9A7A08196F81 CRC64;

  Query Match             15.8%;  Score 235.5;  DB 1;  Length 616;
  Best Local Similarity   31.3%;  Pred. No. 1.9e-11;
  Matches   52;  Conservative   26;  Mismatches   77;  Indels   11;  Gaps    4;

Qy      20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC 76
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Db      47 CNKCEPGKYMSSKCTTTSDSVCLPCGPDEYLDSWNEEDKCLLHKVCDT--GKALVAVVAG 104

Qy      77 HATHNRACRCRTGFF--AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSS 134
           ::|  | | |  |:        |  :  | || |   |   :::| |:||  | || : |
Db     105 NSTTPRRCACTAGYHWSQDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFS 164

Qy     135 SSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           |:::|:|  ||| ||  :   |:   | :|:|     |  | |  |
Db     165 STDKCRPWTNCTFLGKRVEHHGTEKSDAVCSS----SLPARKPPNE 206


Search completed: January  6, 2003, 11:18:40
Job time : 23 secs
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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2003, 11:26:15 ; Search time 51 Seconds
(without alignments)
1629.596 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1491	100.0	1164	2	US-08-794-796-1	Sequence 1, Appli
2	1491	100.0	1347	4	US-09-286-529-18	Sequence 18, Appl
3	1339	89.8	1859	4	US-09-286-529-19	Sequence 19, Appl
4	841	56.4	459	4	US-09-286-529-7	Sequence 7, Appli
5	440.5	29.5	1355	3	US-08-974-022-5	Sequence 5, Appli
6	440.5	29.5	1355	4	US-08-795-445A-5	Sequence 5, Appli
7	440.5	29.5	1355	4	US-08-795-447A-5	Sequence 5, Appli
8	440.5	29.5	1355	4	US-08-974-186-5	Sequence 5, Appli
9	440.5	29.5	1355	4	US-08-795-446B-5	Sequence 5, Appli
10	440.5	29.5	1355	4	US-08-706-945D-127	Sequence 127, App
11	433	29.0	525	3	US-08-997-918-47	Sequence 47, Appl
12	425.5	28.5	2432	3	US-08-974-022-1	Sequence 1, Appli
13	425.5	28.5	2432	4	US-08-795-445A-1	Sequence 1, Appli
14	425.5	28.5	2432	4	US-08-795-447A-1	Sequence 1, Appli
15	425.5	28.5	2432	4	US-08-974-186-1	Sequence 1, Appli
16	425.5	28.5	2432	4	US-08-795-446B-1	Sequence 1, Appli
17	425.5	28.5	2432	4	US-08-706-945D-123	Sequence 123, App
18	424.5	28.5	1324	3	US-08-974-022-3	Sequence 3, Appli
19	424.5	28.5	1324	4	US-08-795-445A-3	Sequence 3, Appli
20	424.5	28.5	1324	4	US-08-795-447A-3	Sequence 3, Appli
21	424.5	28.5	1324	4	US-08-974-186-3	Sequence 3, Appli
22	424.5	28.5	1324	4	US-08-795-446B-3	Sequence 3, Appli
23	424.5	28.5	1324	4	US-08-706-945D-125	Sequence 125, App
24	344.5	23.1	1557	1	US-08-385-229-3	Sequence 3, Appli
25	342	22.9	1641	1	US-08-385-229-1	Sequence 1, Appli
26	342	22.9	1641	2	US-08-650-000-1	Sequence 1, Appli
27	342	22.9	1641	6	5395760-1	Patent No. 5395760
28	342	22.9	2224	4	US-08-477-347-2	Sequence 2, Appli
29	342	22.9	2224	4	US-08-476-862-1	Sequence 1, Appli
30	342	22.9	3683	4	US-09-844-634-3	Sequence 3, Appli
31	340	22.8	705	4	US-09-326-394-3	Sequence 3, Appli
32	338	22.7	705	4	US-09-580-235-1	Sequence 1, Appli
33	338	22.7	705	4	US-09-580-235-7	Sequence 7, Appli
34	338	22.7	705	4	US-09-580-181-1	Sequence 1, Appli
35	338	22.7	705	4	US-09-580-181-7	Sequence 7, Appli
36	338	22.7	705	4	US-09-102-530-1	Sequence 1, Appli
37	338	22.7	705	4	US-09-102-530-7	Sequence 7, Appli
38	337	22.6	705	4	US-09-580-235-3	Sequence 3, Appli
39	337	22.6	705	4	US-09-580-235-5	Sequence 5, Appli
40	337	22.6	705	4	US-09-580-181-3	Sequence 3, Appli
41	337	22.6	705	4	US-09-580-181-5	Sequence 5, Appli
42	337	22.6	705	4	US-09-102-530-3	Sequence 3, Appli
43	337	22.6	705	4	US-09-102-530-5	Sequence 5, Appli
44	332.5	22.3	3796	2	US-08-762-308-11	Sequence 11, Appl
45	332.5	22.3	3796	4	US-09-844-634-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-794-796-1
; Sequence 1, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50000
; TELECOMMUNICATION INFORMATION:

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;      TELEPHONE:  610-270-5219
;      TELEFAX:  610-270-4026
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1164 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-794-796-1

Alignment Scores:
Pred. No.:              1.25e-109      Length:         1164
Score:                  1491.00        Matches:        271
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     2              Gaps:           0

US-09-936-024-1 (1-271) x US-08-794-796-1 (1-1164)

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Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     258 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 317

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db     318 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 377

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db     378 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 437

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     438 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 497

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db     498 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 557

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Db     558 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 617

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     618 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 677

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
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Db     978 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1010

RESULT 2
US-09-286-529-18
; Sequence 18, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 18
;   LENGTH: 1347
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-286-529-18

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Score:                  1491.00        Matches:        271
Percent Similarity:     100.00%        Conservative:   0
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US-09-936-024-1 (1-271) x US-09-286-529-18 (1-1347)

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Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db     765 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 824

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
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Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db   1005 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 1064

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db   1065 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 1124

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db   1185 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1217

RESULT 3
US-09-286-529-19
; Sequence 19, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 1859
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-286-529-19

Alignment Scores:
Pred. No.:                2.69e-97      Length:          1859
Score:                    1339.00       Matches:         271
Percent Similarity:       51.72%        Conservative:    0
Best Local Similarity:    51.72%        Mismatches:      0
Query Match:              89.81%        Indels:          253
DB:                       4             Gaps:            1

US-09-936-024-1 (1-271) x US-09-286-529-19 (1-1859)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 224

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 284

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 344

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 404

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 464

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 524

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 584

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 644

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValPro--------- 177
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCA 704

Qy    177 ------------------------------------------------------------ 177

Db    705 GAGGCCTGAGGGGGCAGCACACTGCAGGCCAGGCCCACTTGTGCCCTCACTCCTGCCCCT 764

Qy    177 ------------------------------------------------------------ 177

Db    765 GCACGTGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGGGGCCACAGTGGATTTG 824

Qy    177 ------------------------------------------------------------ 177

Db    825 AGGGGTCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCTCTCAGGGGTGGCTGAG 884

Qy    177 ------------------------------------------------------------ 177

Db    885 AATTTGGATCTGAGCCAGGGCACAGCCTCCCCTGGAGAGCTCTGGGAAAGTGGGCAGCAA 944

Qy    177 ------------------------------------------------------------ 177

Db    945 TCTCCTAACTGCCCGAGGGGAAGGTGGCTGGCTCCTCTGACACGGGGAAACCGAGGCCTG 1004

Qy    177 ------------------------------------------------------------ 177

Db   1005 ATGGTAATTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTCTGACATGGGGAAACC 1064

Qy    177 ------------------------------------------------------------ 177

Db   1065 GAGGCCCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTGACCCCCTTAACATCAA 1124

Qy    177 ------------------------------------------------------------ 177

Db   1125 GTCAGGTCCGGTCCATCTGCAGGTCCCAACTCGCCCCTTCCGATGGCCCAGGAGCCCCAA 1184

Qy    177 ------------------------------------------------------------ 177

Db   1185 GCCCTTGCCTGGGCCCCCTTGCCTCTTGCAGCCAAGGTCCGAGTGGCCGCTCCTGCCCCC 1244

Qy    177 ------------------------------------------------------------ 177

Db   1245 TAGGCCTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCTTCTCCAGTCCCCATCGTT 1304

Qy    177 ------------------------------------------------------------ 177

Db   1305 GCACTGCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTCCTGCAAACCCCCCG 1364

Qy    177 ------------------------------------------------------------ 177

Db   1365 AGTGGGGCCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAGTGTGTGTGGGTGAAATGAT 1424

Qy    178 ----------------------------GlyAlaGluGluCysGluArgAlaValIleAs 188
                                       ||||||||||||||||||||||||||||||||
Db   1425 CGGACCGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGA 1484

Qy    188 pPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGl 208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1485 CTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGA 1544

Qy    208 uAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLe 228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1545 GGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCT 1604

Qy    228 uArgArgArgLeuThrGluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuLe 248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1605 GCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCT 1664

Qy    248 uGlnAlaLeuArgValAlaArgMetProGlyLeuGluArgSerValArgGluArgPheLe 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1665 GCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCT 1724

Qy    268 uProValHis 271
          ||||||||||
Db   1725 CCCTGTGCAC 1734

RESULT 4
US-09-286-529-7
; Sequence 7, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 459
;   TYPE: DNA
;   ORGANISM: human
US-09-286-529-7

Alignment Scores:
Pred. No.:          1.21e-58      Length:          459
Score:              841.00        Matches:         153
Percent Similarity: 100.00%       Conservative:    0
Best Local Similarity: 100.00%    Mismatches:      0
Query Match:        56.41%        Indels:          0
DB:                 4             Gaps:            0

US-09-936-024-1 (1-271) x US-09-286-529-7 (1-459)

Qy     56 LeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAla 75
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCT 60

Qy     76 CysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGly 95
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGT 120

Qy     96 PheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrPro 115
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC 180

Qy    116 SerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSer 135
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGC 240

Qy    136 SerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPro 155
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCA 300

Qy    156 GlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArg 175
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGG 360

Qy    176 ValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIle 195
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATC 420

Qy    196 SerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGlu 208
          |||||||||||||||||||||||||||||||||||||
Db    421 TCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAG 459

RESULT 5
US-08-974-022-5
; Sequence 5, Application US/08974022
; Patent No. 6015938
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,022
;      FILING DATE:  12-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1355 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  94..1296
US-08-974-022-5

Alignment Scores:
Pred. No.:          3.05e-26      Length:          1355
Score:              440.50        Matches:         77
Percent Similarity: 57.75%        Conservative:    31
Best Local Similarity: 41.18%     Mismatches:      74
Query Match:        29.54%        Indels:          5
DB:                 3             Gaps:            2

US-09-936-024-1 (1-271) x US-08-974-022-5 (1-1355)

Qy      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
          |||   |||         |||   ||||||      :::|||:::|||   :::||||||
Db    169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT 228

Qy     25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
          |||||||||:::::::::::   |||                |||   |||   ||||||
Db    229 CCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC 288

Qy     45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
          |||      :::||||||      |||:::      :::  |||  ||||||:::
Db    289 CCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCC 348

Qy     65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
          :::|||   |||  :::         :::   |||:::  ||||||||||||   |||
Db    349 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGC 408

Qy     85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
             |||:::   |||  :::            |||||||||:::|||   ||||||||||
Db    409 GAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCT 468

Qy    105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
          ||||||   ||||||:::      |||||||||   :::|||||||   |||:::   |||
Db    469 CCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGT 528

Qy    125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
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          ||| ||| |||||| :::|||||| |||::: ||| |||
Db    529 CCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAAT 588

Qy    145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
          |||::: |||||| ||| |||::::::::::|||||| :::
Db    589 TGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATA--- 645

Qy    165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu------Cys 182
              |||:::||| |||||::: ||| ::: |||
Db    646 ------TGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGT 699

Qy    183 GluArgAlaValIleAspPhe 189
          ||| ||| |||
Db    700 GAGGAGGCATTCTTCAGGTTT 720

RESULT 6
US-08-795-445A-5
; Sequence 5, Application US/08795445A
; Patent No. 6284485
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,445A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1355 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  94..1296
US-08-795-445A-5

Alignment Scores:
Pred. No.:              3.05e-26      Length:          1355
Score:                  440.50        Matches:         77
Percent Similarity:     57.75%        Conservative:    31
Best Local Similarity:  41.18%        Mismatches:      74
Query Match:            29.54%        Indels:          5
DB:                     4             Gaps:            2

US-09-936-024-1 (1-271) x US-08-795-445A-5 (1-1355)

Qy      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
          ||| ||| ||| ||||||  :::|||:::||| :::||||||
Db    169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT 228

Qy     25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
          |||||||||:::::::::::  |||  ||| ||| |||||||
Db    229 CCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC 288

Qy     45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
          |||  :::|||||  |||:::  :::  |||  ||||||:::
Db    289 CCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCC 348

Qy     65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
          :::|||  |||  :::  :::  |||:::  ||||||||||  |||
Db    349 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGC 408

Qy     85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
             |||:::  |||  :::  |||||||||:::|||  |||||||||
Db    409 GAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCT 468

Qy    105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
          ||||||  ||||||:::  |||||||||  :::||||||  |||:::  |||  |||
Db    469 CCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGT 528

Qy    125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
          |||  |||  ||||||  :::||||||  |||:::  |||  |||
Db    529 CCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAAT 588

Qy    145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
          |||:::  ||||||  |||  |||:::::::::||||||  :::
Db    589 TGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATA--- 645

Qy    165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu------Cys 182
              |||:::||| |||||::: ||| ::: |||
Db    646 ------TGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGT 699

Qy    183 GluArgAlaValIleAspPhe 189
          ||| ||| |||
Db    700 GAGGAGGCATTCTTCAGGTTT 720

RESULT 7
US-08-795-447A-5
; Sequence 5, Application US/08795447A
; Patent No. 6284728
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, William J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  Osteoprotegerin
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  One Amgen Center Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91362-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,447A
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378D2
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1355 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  94..1296
US-08-795-447A-5

Alignment Scores:
Pred. No.:              3.05e-26        Length:         1355
Score:                  440.50          Matches:        77
Percent Similarity:     57.75%          Conservative:   31
Best Local Similarity:  41.18%          Mismatches:     74
Query Match:            29.54%          Indels:         5
DB:                     4               Gaps:           2

US-09-936-024-1 (1-271) x US-08-795-447A-5 (1-1355)

Qy      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
          |||   |||         |||   ||||||      :::|||:::|||   :::||||||
Db    169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT 228

Qy     25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
          |||||||||:::::::::::::   |||                |||   |||   ||||||
Db    229 CCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC 288

Qy     45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
          |||       :::||||||      |||:::      :::   |||   ||||||:::
Db    289 CCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCC 348

Qy     65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
          :::|||   |||   :::         :::   |||:::   ||||||||||||   |||
Db    349 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGC 408

Qy     85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
            |||:::   |||   :::             |||||||||:::|||   |||||||||
Db    409 GAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCT 468

Qy    105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
          ||||||   ||||||:::      |||||||||   :::|||||   |||:::   |||
Db    469 CCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGT 528

Qy    125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
          |||   |||   ||||||      :::|||||          |||:::   |||   |||
Db    529 CCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAAT 588

Qy    145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
          |||:::      ||||||   |||         |||:::::::::||||||   :::
Db    589 TGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATA--- 645

Qy    165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu------Cys 182
            |||:::|||         ||||||:::      |||   :::          |||
Db    646 ------TGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGT 699

Qy    183 GluArgAlaValIleAspPhe 189
          |||   |||         |||
Db    700 GAGGAGGCATTCTTCAGGTTT 720

RESULT 8
US-08-974-186-5
; Sequence 5, Application US/08974186
; Patent No. 6284740
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1355 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  94..1296
US-08-974-186-5

Alignment Scores:
Pred. No.:              3.05e-26        Length:         1355
Score:                  440.50          Matches:        77
Percent Similarity:     57.75%          Conservative:   31
Best Local Similarity:  41.18%          Mismatches:     74
Query Match:            29.54%          Indels:         5
DB:                     4               Gaps:           2

US-09-936-024-1 (1-271) x US-08-974-186-5 (1-1355)

Qy      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
          |||   |||         |||   ||||||      :::|||:::|||   :::||||||
Db    169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT 228

Qy     25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
          |||||||||:::::::::::::   |||                |||   |||   ||||||
Db    229 CCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC 288

Qy     45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
          |||       :::||||||      |||:::      :::   |||   ||||||:::
Db    289 CCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCC 348

Qy     65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
          :::|||   |||   :::         :::   |||:::   ||||||||||||   |||
Db    349 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGC 408

Qy     85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
            |||:::   |||   :::             |||||||||:::|||   |||||||||
Db    409 GAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCT 468

Qy    105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
          ||||||   ||||||:::      |||||||||   :::|||||   |||:::   |||
Db    469 CCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGT 528

Qy    125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
          |||   |||   ||||||      :::|||||          |||:::   |||   |||
Db    529 CCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAAT 588

Qy    145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
          |||:::      ||||||   |||         |||:::::::::||||||   :::
Db    589 TGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATA--- 645

Qy    165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu------Cys 182
            |||:::|||         ||||||:::      |||   :::          |||
Db    646 ------TGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGT 699
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Qy    183 GluArgAlaValIleAspPhe 189
          |||   |||         |||
Db    700 GAGGAGGCATTCTTCAGGTTT 720

RESULT 9
US-08-795-446B-5
; Sequence 5, Application US/08795446B
; Patent No. 6288032
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,446B
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1355 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  94..1296
US-08-795-446B-5

Alignment Scores:
Pred. No.:              3.05e-26      Length:          1355
Score:                  440.50        Matches:         77
Percent Similarity:     57.75%        Conservative:    31
Best Local Similarity:  41.18%        Mismatches:      74
Query Match:            29.54%        Indels:          5
DB:                     4             Gaps:            2

US-09-936-024-1 (1-271) x US-08-795-446B-5 (1-1355)

Qy      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
          |||   |||         |||   ||||||      :::|||:::|||   :::||||||
Db    169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT 228

Qy     25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
          |||||||||:::::::::::::   |||                |||   |||   ||||||
Db    229 CCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC 288

Qy     45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
          |||      :::|||||||      |||:::      :::   |||   ||||||:::
Db    289 CCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCC 348

Qy     65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
          :::|||   |||   :::         :::   |||:::   ||||||||||||   |||
Db    349 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGC 408

Qy     85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
          |||:::   |||   :::           |||||||||:::|||   |||||||||
Db    409 GAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCT 468

Qy    105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
          ||||||   ||||||:::      |||||||||   :::||||||   |||:::   |||
Db    469 CCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGT 528

Qy    125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
          |||   |||   ||||||       :::||||||           |||:::   |||   |||
Db    529 CCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAAT 588

Qy    145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
          |||:::      ||||||   |||         |||:::::::::||||||   :::
Db    589 TGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATA--- 645

Qy    165 ThrSerCysThrGlyProLeuSerThrArgValProGlyAlaGluGlu------Cys 182
                |||:::|||         ||||||:::      |||   :::         |||
Db    646 ------TGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGT 699

Qy    183 GluArgAlaValIleAspPhe 189
          |||   |||         |||
Db    700 GAGGAGGCATTCTTCAGGTTT 720

RESULT 10
US-08-706-945D-127
; Sequence 127, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Lacey, David
;  APPLICANT:  Calzone, Frank
;  APPLICANT:  Chang, Ming-Shi
;  TITLE OF INVENTION: Osteoprotegerin
;  FILE REFERENCE: A-378CIP
;  CURRENT APPLICATION NUMBER: US/08/706,945D
;  CURRENT FILING DATE:  1996-09-03
;  PRIOR APPLICATION NUMBER: 08/577,788
;  PRIOR FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 145
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
;   LENGTH: 1355
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (94)..(1296)
;   OTHER INFORMATION:
US-08-706-945D-127

Alignment Scores:
Pred. No.:              3.05e-26      Length:          1355
Score:                  440.50        Matches:         77
Percent Similarity:     57.75%        Conservative:    31
Best Local Similarity:  41.18%        Mismatches:      74
Query Match:            29.54%        Indels:          5
DB:                     4             Gaps:            2

US-09-936-024-1 (1-271) x US-08-706-945D-127 (1-1355)

Qy      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
          |||   |||         |||   ||||||      :::|||:::|||   :::||||||
Db    169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT 228

Qy     25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
          |||||||||:::::::::::::   |||                |||   |||   ||||||
Db    229 CCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC 288

Qy     45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
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Db    289 CCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCC 348

Qy     65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84

Db    349 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGC 408

Qy     85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104

Db    409 GAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCT 468

Qy    105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124

Db    469 CCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGT 528

Qy    125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144

Db    529 CCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAAT 588

Qy    145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164

Db    589 TGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATA--- 645

Qy    165 ThrSerCysThrGlyProLeuSerThrArgValProGlyAlaGluGlu------Cys 182

Db    646 ------TGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGT 699

Qy    183 GluArgAlaValIleAspPhe 189

Db    700 GAGGAGGCATTCTTCAGGTTT 720

RESULT 11
US-08-997-918-47
; Sequence 47, Application US/08997918
; Patent No. 6077689
; GENERAL INFORMATION:
;  APPLICANT: Snavely, Marshall D.
;  TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS
;  FILE REFERENCE: A-496
;  CURRENT APPLICATION NUMBER: US/08/997,918
;  CURRENT FILING DATE: 1997-12-24
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: fragment encoding amino acids 22-194 of human OPG
US-08-997-918-47

Alignment Scores:
Pred. No.:              3.25e-26      Length:          525
Score:                  433.00        Matches:         69
Percent Similarity:     60.87%        Conservative:    29
Best Local Similarity:  42.86%        Mismatches:      63
Query Match:            29.04%        Indels:          0
DB:                     3             Gaps:            0

US-09-936-024-1 (1-271) x US-08-997-918-47 (1-525)

Qy      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24

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Qy     25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44

Db     76 CCGGGTACCTACCTGAAACAGCACTGCACCGCTAAATGGAAAACCGTTTGCGCTCCTTGT 135

Qy     45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64

Db    136 CCGGACCACTACTACACCGACTCCTGGCACACCTCCGACGAATGCCTGTACTGCTCACCG 195

Qy     65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84

Db    196 GTTTGCAAGGAGCTGCAGTACGTTAAACAGGAATGCAACCGTACGCACAACCGTGTATGC 255

Qy     85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104

Db    256 GAATGCAAAGAAGGTCGTTACCTGGAGATCGAATTCTGCCTGAAACACCGTTCCTGTCCG 315

Qy    105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124

Db    316 CCTGGTTTCGGTGTTGTACAGGCTGGTACCCCGGAACGTAACACCGTTTGCAAACGTTGC 375

Qy    125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144

Db    376 CCGGACGGTTTCTTCTCCAACGAAACCTCGAGCAAAGCTCCGTGCCGTAAACACACCAAC 435

Qy    145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164

Db    436 TGCTCCGTTTTCGGTCTCCTGTTAACCCAGAAAGGTAACGCTACCCACGACAACATCTGC 495

Qy    165 Thr 165

Db    496 TCC 498

RESULT 12
US-08-974-022-1
; Sequence 1, Application US/08974022
; Patent No. 6015938
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,022
;      FILING DATE:  12-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  124..1326
US-08-974-022-1

Alignment Scores:
Pred. No.:              1.06e-24      Length:          2432
Score:                  425.50        Matches:         81
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Percent Similarity:     55.61%          Conservative:  33
Best Local Similarity:  39.51%          Mismatches:    86
Query Match:            28.54%          Indels:        5
DB:                     3               Gaps:          2

US-09-936-024-1 (1-271) x US-08-974-022-1 (1-2432)

Qy       5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
           |||   |||         |||   |||||||||   :::|||:::|||   :::|||
Db     199 CCAAAATACTTGCATTATGACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCT 258

Qy      25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
           |||||||||:::::::::::::   |||                |||   |||   ||||||
Db     259 CCTGGCACCTACCTAAAACAGCACTGCACAGTCAGGAGGAAGACACTGTGTGTCCCTTGC 318

Qy      45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
           |||         ||||||      |||:::      :::   |||   ||||||:::
Db     319 CCTGACTACTCTTATACAGACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCC 378

Qy      65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
           :::|||   |||   :::         :::   |||:::   ||||||||||||   |||
Db     379 GTGTGCAAGGAACTGCAGACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGC 438

Qy      85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
             |||      |||   :::             |||||||||:::|||   |||||||||
Db     439 GAATGTGAGGAAGGGCGCTACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCC 498

Qy     105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
           ||||||   ||||||:::      |||||||||   :::||||||   |||:::   |||
Db     499 CCAGGCTTGGGTGTGCTGCAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGT 558

Qy     125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
           |||   |||   ||||||      :::||||||          |||:::   |||   |||
Db     559 CCGGATGGGTTCTTCTCAGGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAAC 618

Qy     145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
           |||::::::|||||||||   |||         |||:::::::::|||||   :::
Db     619 TGCAGCTCACTTGGCCTCCTGCTAATTCAGAAAGGAAATGCAACACATGACAATGTA--- 675

Qy     165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu------Cys 182
                |||:::|||         :::|||:::      |||   :::          |||
Db     676 ------TGTTCCGGAAACAGAGAAGCAACTCAAAATTGTGGAATAGATGTCACCCTGTGC 729

Qy     183 GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArg 202
           |||   |||         |||                 |||                |||
Db     730 GAAGAGGCATTCTTCAGGTTTGCTGTGCCTACCAAGATTATACCGAATTGGCTGAGTGTT 789

Qy     203 LeuLeuGlnAlaLeu 207
           |||:::   :::|||
Db     790 CTGGTGGACAGTTTG 804

RESULT 13
US-08-795-445A-1
; Sequence 1, Application US/08795445A
; Patent No. 6284485
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,445A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  124..1326
US-08-795-445A-1

Alignment Scores:
Pred. No.:              1.06e-24        Length:        2432
Score:                  425.50          Matches:       81
Percent Similarity:     55.61%          Conservative:  33
Best Local Similarity:  39.51%          Mismatches:    86
Query Match:            28.54%          Indels:        5
DB:                     4               Gaps:          2

US-09-936-024-1 (1-271) x US-08-795-445A-1 (1-2432)

Qy       5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
           |||   |||         |||   |||||||||   :::|||:::|||   :::|||
Db     199 CCAAAATACTTGCATTATGACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCT 258

Qy      25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
           |||||||||:::::::::::::   |||                |||   |||   ||||||
Db     259 CCTGGCACCTACCTAAAACAGCACTGCACAGTCAGGAGGAAGACACTGTGTGTCCCTTGC 318

Qy      45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
           |||         ||||||      |||:::      :::   |||   ||||||:::
Db     319 CCTGACTACTCTTATACAGACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCC 378

Qy      65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
           :::|||   |||   :::         :::   |||:::   ||||||||||||   |||
Db     379 GTGTGCAAGGAACTGCAGACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGC 438

Qy      85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
             |||      |||   :::             |||||||||:::|||   |||||||||
Db     439 GAATGTGAGGAAGGGCGCTACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCC 498

Qy     105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
           ||||||   ||||||:::      |||||||||   :::||||||   |||:::   |||
Db     499 CCAGGCTTGGGTGTGCTGCAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGT 558

Qy     125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
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Db     559 CCGGATGGGTTCTTCTCAGGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAAC 618

Qy     145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
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Db     619 TGCAGCTCACTTGGCCTCCTGCTAATTCAGAAAGGAAATGCAACACATGACAATGTA--- 675

Qy     165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu------Cys 182
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Db     676 ------TGTTCCGGAAACAGAGAAGCAACTCAAAATTGTGGAATAGATGTCACCCTGTGC 729

Qy     183 GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArg 202
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Db     730 GAAGAGGCATTCTTCAGGTTTGCTGTGCCTACCAAGATTATACCGAATTGGCTGAGTGTT 789
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Qy    203 LeuLeuGlnAlaLeu 207
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Db    790 CTGGTGGACAGTTTG 804

RESULT 14
US-08-795-447A-1
; Sequence 1, Application US/08795447A
; Patent No. 6284728
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, William J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  Osteoprotegerin
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  One Amgen Center Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91362-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,447A
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378D2
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  124..1326
US-08-795-447A-1

Alignment Scores:
Pred. No.:              1.06e-24      Length:          2432
Score:                  425.50        Matches:         81
Percent Similarity:     55.61%        Conservative:    33
Best Local Similarity:  39.51%        Mismatches:      86
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DB:                     4             Gaps:            2

US-09-936-024-1 (1-271) x US-08-795-447A-1 (1-2432)

Qy      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
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Db    199 CCAAAATACTTGCATTATGACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCT 258

Qy     25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
          |||||||||:::::::::::   |||                |||   |||   ||||||
Db    259 CCTGGCACCTACCTAAAACAGCACTGCACAGTCAGGAGGAAGACACTGTGTGTCCCTTGC 318

Qy     45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
          |||         ||||||      |||:::      :::   |||   ||||||:::
Db    319 CCTGACTACTCTTATACAGACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCC 378

Qy     65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
          :::|||   |||   :::         :::   |||:::   ||||||||||||   |||
Db    379 GTGTGCAAGGAACTGCAGACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGC 438

Qy     85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
             |||       |||   :::           |||||||||:::|||   |||||||||
Db    439 GAATGTGAGGAAGGGCGCTACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCC 498

Qy    105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
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Db    499 CCAGGCTTGGGTGTGCTGCAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGT 558

Qy    125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
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Qy    165 ThrSerCysThrGlyProLeuSerThrArgValProGlyAlaGluGlu------Cys 182
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Qy    203 LeuLeuGlnAlaLeu 207
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Db    790 CTGGTGGACAGTTTG 804

RESULT 15
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; Sequence 1, Application US/08974186
; Patent No. 6284740
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  124..1326
US-08-974-186-1

Alignment Scores:
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Pred. No.:	1.06e-24	Length:	2432
Score:	425.50	Matches:	81
Percent Similarity:	55.61%	Conservative:	33
Best Local Similarity:	39.51%	Mismatches:	86
Query Match:	28.54%	Indels:	5
DB:	4	Gaps:	2

US-09-936-024-1 (1-271) x US-08-974-186-1 (1-2432)

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Db     199 CCAAAATACTTGCATTATGACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCT 258

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Qy      45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
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Db     319 CCTGACTACTCTTATACAGACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCC 378

Qy      65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
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Db     379 GTGTGCAAGGAACTGCAGACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGC 438

Qy      85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
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Db     439 GAATGTGAGGAAGGGCGCTACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCC 498

Qy     105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
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Db     499 CCAGGCTTGGGTGTGCTGCAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGT 558

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Db     559 CCGGATGGGTTCTTCTCAGGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAAC 618

Qy     145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
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Qy     165 ThrSerCysThrGlyProProLeuSerThrArgValProGlyAlaGluGlu------Cys 182
                |||:::|||         :::|||:::      |||   :::         |||
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Db     730 GAAGAGGCATTCTTCAGGTTTGCTGTGCCTACCAAGATTATACCGAATTGGCTGAGTGTT 789

Qy     203 LeuLeuGlnAlaLeu 207
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GenCore version 5.1.3
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Run on: January 6, 2003, 11:31:16 ; Search time 132 Seconds
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887.945 Million cell updates/sec

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Searched: 381593 seqs, 216252194 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1491	100.0	1077	10	US-09-935-727-1	Sequence 1, Appli
3	1491	100.0	1114	10	US-09-896-096A-2	Sequence 2, Appli
4	1491	100.0	1114	10	US-09-894-924-2	Sequence 2, Appli
5	1491	100.0	1347	10	US-09-877-156-18	Sequence 18, Appl
6	1491	100.0	1550	10	US-09-935-727-33	Sequence 33, Appl
7	1469	98.5	1137	10	US-09-840-795-1	Sequence 1, Appli
8	1339	89.8	1859	10	US-09-877-156-19	Sequence 19, Appl
9	1287.5	86.4	1796	10	US-09-935-727-28	Sequence 28, Appl
10	982.5	65.9	1667	10	US-09-935-727-3	Sequence 3, Appli
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13	841	56.4	459	10	US-09-877-156-7	Sequence 7, Appli
14	461	30.9	981	10	US-09-062-113-92	Sequence 92, Appl
15	442.5	29.7	1206	10	US-09-062-113-83	Sequence 83, Appl
16	440.5	29.5	819	10	US-09-062-113-96	Sequence 96, Appl
17	440.5	29.5	966	10	US-09-062-113-101	Sequence 101, App
18	440.5	29.5	984	10	US-09-062-113-93	Sequence 93, Appl
19	440.5	29.5	1056	10	US-09-062-113-95	Sequence 95, Appl
20	440.5	29.5	1089	10	US-09-062-113-10	Sequence 10, Appl
21	440.5	29.5	1182	10	US-09-062-113-100	Sequence 100, App
22	440.5	29.5	1200	10	US-09-062-113-94	Sequence 94, Appl
23	440.5	29.5	1203	12	US-10-105-934-3	Sequence 3, Appli
24	440.5	29.5	1206	10	US-09-062-113-6	Sequence 6, Appli
25	440.5	29.5	1206	10	US-09-062-113-85	Sequence 85, Appl
26	440.5	29.5	1206	10	US-09-062-113-86	Sequence 86, Appl
27	440.5	29.5	1206	10	US-09-062-113-87	Sequence 87, Appl
28	440.5	29.5	1356	10	US-09-954-456-1164	Sequence 1164, Ap
29	440.5	29.5	1527	12	US-10-164-592-1	Sequence 1, Appli
30	440.5	29.5	2122	12	US-10-105-934-14	Sequence 14, Appl
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32	440.5	29.5	2139	10	US-09-765-231A-4	Sequence 4, Appli
33	433.5	29.1	1206	10	US-09-062-113-84	Sequence 84, Appl
34	433	29.0	564	10	US-09-062-113-102	Sequence 102, App
35	433	29.0	594	10	US-09-062-113-97	Sequence 97, Appl
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43	380	25.5	499	10	US-09-935-727-17	Sequence 17, Appl
44	365	24.5	226	10	US-09-896-096A-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-09-935-727-32
; Sequence 32, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12

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;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 903
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Mammalian synthetic TNFR-6 alpha
US-09-935-727-32

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Best Local Similarity:    100.00%        Mismatches:      0
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Db     148 GCTCAGTGTCCTCCTGGAACATTTGTGCAAAGGCCTTGTAGGCGCGATTCTCCTACGACG 207

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db     208 TGTGGCCCTTGCCCTCCTAGGCACTATACACAGTTTTGGAACTATCTCGAGCGCTGTAGG 267

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Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Db     628 GAGTGCGAACGCGCTGTGATCGACTTTGTGGCCTTCCAGGATATCTCTATCAAAAGGCTG 687

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 CAACGCCTGCTGCAAGCTCTGGAAGCTCCTGAGGGCTGGGGTCCCACACCAAGGGCTGGC 747

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 AGGGCTGCACTGCAACTGAAGCTTCGCAGGAGGCTCACTGAACTCCTGGGAGCTCAAGAT 807

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 GGAGCTCTGCTGGTGAGGCTGCTGCAAGCTCTGAGGGTGGCAAGGATGCCTGGACTGGAG 867

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
           |||||||||||||||||||||||||||||||
Db     868 CGCTCTGTGAGGGAACGCTTCCTGCCTGTGCAC 900

RESULT 2
US-09-935-727-1
; Sequence 1, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1077
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(924)
US-09-935-727-1

Alignment Scores:
Pred. No.:                3.99e-106      Length:          1077
Score:                    1491.00        Matches:         271
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       10             Gaps:            0

US-09-936-024-1 (1-271) x US-09-935-727-1 (1-1077)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 171

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 231

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    232 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 291

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 351

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    352 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 411

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    412 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 471

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    472 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 531

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    532 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 591

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    592 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 651

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    652 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 711

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    712 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 771

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    772 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 831

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    832 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 891

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          ||||||||||||||||||||||||||||||||
Db    892 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 924

RESULT 3
US-09-896-096A-2
; Sequence 2, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/896,096A
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 2
;   LENGTH: 1114
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: 1090
;   OTHER INFORMATION: Unknown base
US-09-896-096A-2

Alignment Scores:
Pred. No.:              4.15e-106       Length:         1114
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-09-936-024-1 (1-271) x US-09-896-096A-2 (1-1114)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    188 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 247

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 307

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 427

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 607

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    608 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 667

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    668 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 727

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    728 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 787

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    788 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 847

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    848 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 907

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    908 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 967

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
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          ||||||||||||||||||||||||||||||||
Db    968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000

RESULT 4
US-09-894-924-2
; Sequence 2, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/894,924
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 2
;   LENGTH: 1114
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: 1090
;   OTHER INFORMATION: Unknown base
US-09-894-924-2

Alignment Scores:
Pred. No.:              4.15e-106      Length:          1114
Score:                  1491.00        Matches:         271
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     10             Gaps:            0

US-09-936-024-1 (1-271) x US-09-894-924-2 (1-1114)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     188 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 247

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     248 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 307

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     308 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     368 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 427

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     548 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 607

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     608 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 667

Qy     161 AspThrLeuCysThrSerCysThrGlyProProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     668 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 727

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     728 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 787

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     788 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 847

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     848 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 907

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     908 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 967

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db     968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000

RESULT 5
US-09-877-156-18
; Sequence 18, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
;  APPLICANT: Catherine Tribouley
;  TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE: 1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/877,156
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/286,529
;  PRIOR FILING DATE: 1998-04-05
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
;   LENGTH: 1347
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-877-156-18

Alignment Scores:
Pred. No.:              5.21e-106      Length:          1347
Score:                  1491.00        Matches:         271
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     10             Gaps:            0

US-09-936-024-1 (1-271) x US-09-877-156-18 (1-1347)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     405 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 464

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     465 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 524

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     525 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 584
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Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     585 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 644

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     645 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 704

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     705 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 764

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     765 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 824

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     825 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 884

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     885 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 944

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     945 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 1004

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1005 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 1064

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1065 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 1124

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1125 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 1184

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
           |||||||||||||||||||||||||||||||
Db    1185 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1217

RESULT 6
US-09-935-727-33
; Sequence 33, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
;   LENGTH: 1550
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Codon optimized TNFR-6 alpha
US-09-935-727-33

Alignment Scores:
Pred. No.:              6.16e-106      Length:          1550
Score:                  1491.00        Matches:         271
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     10             Gaps:            0

US-09-936-024-1 (1-271) x US-09-935-727-33 (1-1550)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     738 GTTGCTGAAACACCAACTATACCCATGGAGAGATGCTGAAACTGGTGAAAGACTGGTTTGT 797

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     798 GCTCAATGTCCACCAGGTACTTTTGTTCAAAGACCATGTAGAAGAGATTCTCCAACTACT 857

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     858 TGTGGTCCATGTCCACCAAGACATTACACTCAATTTTGGAACTACCTGGAAAGATGTAGA 917

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     918 TACTGTAACGTTCTTTGTGGTGAAAGAGAAGAAGAAGCTAGAGCTTGTCATGCTACTCAT 977

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     978 AACAGAGCTTGTAGATGTAGAACTGGTTTTTTTGCTCATGCTGGTTTTTGTTTGGAACAT 1037

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1038 GCTTCTTGTCCACCTGGTGCTGGTGTTATTGCTCCTGGTACTCCTTCTCAAAACACTCAA 1097

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1098 TGTCAGCCATGTCCACCAGGTACTTTTTCTGCTTCTTCTTCTTCTTCTGAACAATGTCAA 1157

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1158 CCACATAGAAACTGTACTGCTTTGGGTCTGGCTTTGAATGTTCCAGGTTCTTCTTCTCAT 1217

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1218 GATACTTTGTGTACTTCTTGTACTGGTTTTCCTTTGTCTACTAGAGTTCCAGGTGCTGAA 1277

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1278 GAATGTGAAAGAGCTGTTATTGATTTTGTTGCTTTTCAAGATATTTCTATTAAGAGACTG 1337

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1338 CAAAGACTGCTGCAAGCTCTGGAAGCTCCAGAAGGTTGGGGTCCAACTCCAAGAGCTGGT 1397

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1398 AGAGCTGCTTTGCAATTGAAGTTGAGAAGAAGATTGACAGAATTGTTGGGTGCTCAAGAT 1457
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Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 GGTGCTTTGTTGGTTAGATTGTTGCAAGCTTTGAGAGTTGCTAGAATGCCTGGTTTGGAA 1517

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db   1518 AGATCTGTTAGAGAAAGATTTTTGCCAGTTCAC 1550

RESULT 7
US-09-840-795-1
; Sequence 1, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Erin E.
;  APPLICANT:  Mattson, Jeanine D.
;  APPLICANT:  Bates, Elizabeth Esther Mary
;  APPLICANT:  Gorman, Daniel M.
;  APPLICANT:  Lebecque, Serge J.E.
;  TITLE OF INVENTION: Mammalian Genes; Related Reagents
;  FILE REFERENCE: SF0818K
;  CURRENT APPLICATION NUMBER: US/09/840,795
;  CURRENT FILING DATE:  2001-04-23
;  PRIOR APPLICATION NUMBER: 09/351,777
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1137
;   TYPE: DNA
;   ORGANISM: primate
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (99)..(998)
;   NAME/KEY: misc_feature
;   LOCATION: (367)
;   OTHER INFORMATION: W; may be A or T
;   NAME/KEY: mat_peptide
;   LOCATION: (132)..(998)
US-09-840-795-1

Alignment Scores:
Pred. No.:              2.06e-104       Length:         1137
Score:                  1469.00         Matches:        268
Percent Similarity:     98.89%          Conservative:   0
Best Local Similarity:  98.89%          Mismatches:     3
Query Match:            98.52%          Indels:         0
DB:                     10              Gaps:           0

US-09-936-024-1 (1-271) x US-09-840-795-1 (1-1137)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 245

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db    246 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCATGACG 305

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 365

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
             |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TWCTGCTACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 425

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 485

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 545

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 605

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 665

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 725

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 785

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 845

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 905

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 965

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db    966 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 998

RESULT 8
US-09-877-156-19
; Sequence 19, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
;  APPLICANT: Catherine Tribouley
;  TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE: 1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/877,156
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/286,529
;  PRIOR FILING DATE: 1998-04-05
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 1859
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-877-156-19

Alignment Scores:
Pred. No.:              3.37e-94        Length:         1859
Score:                  1339.00         Matches:        271
Percent Similarity:     51.72%          Conservative:   0
Best Local Similarity:  51.72%          Mismatches:     0
Query Match:            89.81%          Indels:         253
DB:                     10              Gaps:           1

US-09-936-024-1 (1-271) x US-09-877-156-19 (1-1859)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 224

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 284

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    285 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 344

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80

Db    345 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 404

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100

Db    405 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 464

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120

Db    465 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 524

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140

Db    525 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 584

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160

Db    585 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 644

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValPro--------- 177

Db    645 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCA 704

Qy    177 ------------------------------------------------------------ 177

Db    705 GAGGCCTGAGGGGGCAGCACACTGCAGGCCAGGCCCACTTGTGCCCTCACTCCTGCCCCT 764

Qy    177 ------------------------------------------------------------ 177

Db    765 GCACGTGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGGGGCCACAGTGGATTTG 824

Qy    177 ------------------------------------------------------------ 177

Db    825 AGGGGTCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCTCTCAGGGGTGGCTGAG 884

Qy    177 ------------------------------------------------------------ 177

Db    885 AATTTGGATCTGAGCCAGGGCACAGCCTCCCCTGGAGAGCTCTGGGAAAGTGGGCAGCAA 944

Qy    177 ------------------------------------------------------------ 177

Db    945 TCTCCTAACTGCCCGAGGGGAAGGTGGCTGGCTCCTCTGACACGGGGAAACCGAGGCCTG 1004

Qy    177 ------------------------------------------------------------ 177

Db   1005 ATGGTAATTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTCTGACATGGGGAAACC 1064

Qy    177 ------------------------------------------------------------ 177

Db   1065 GAGGCCCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTGACCCCCTTAACATCAA 1124

Qy    177 ------------------------------------------------------------ 177

Db   1125 GTCAGGTCCGGTCCATCTGCAGGTCCCAACTCGCCCCTTCCGATGGCCCAGGAGCCCCAA 1184

Qy    177 ------------------------------------------------------------ 177

Db   1185 GCCCTTGCCTGGGCCCCCTTGCCTCTTGCAGCCAAGGTCCGAGTGGCCGCTCCTGCCCCC 1244

Qy    177 ------------------------------------------------------------ 177

Db   1245 TAGGCCTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCTTCTCCAGTCCCCATCGTT 1304

Qy    177 ------------------------------------------------------------ 177

Db   1305 GCACTGCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTCCTGCAAACCCCCCG 1364

Qy    177 ------------------------------------------------------------ 177

Db   1365 AGTGGGGCCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAGTGTGTGTGGGTGAAATGAT 1424

Qy    178 ----------------------------GlyAlaGluGluCysGluArgAlaValIleAs 188

Db   1425 CGGACCGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGA 1484

Qy    188 pPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGl 208

Db   1485 CTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGA 1544

Qy    208 uAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLe 228

Db   1545 GGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCT 1604

Qy    228 uArgArgArgLeuThrGluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuLe 248

Db   1605 GCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCT 1664

Qy    248 uGlnAlaLeuArgValAlaArgMetProGlyLeuGluArgSerValArgGluArgPheLe 268

Db   1665 GCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCT 1724

Qy    268 uProValHis 271

Db   1725 CCCTGTGCAC 1734
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RESULT 9
US-09-935-727-28
; Sequence 28, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: intron
; LOCATION: 425-560
; NAME/KEY: intron
; LOCATION: 756-1512
US-09-935-727-28

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Alignment Scores:
Pred. No.:                2.85e-90        Length:          1796
Score:                    1287.50         Matches:         271
Percent Similarity:       47.54%          Conservative:    0
Best Local Similarity:    47.54%          Mismatches:      0
Query Match:              86.35%          Indels:          299
DB:                       10              Gaps:            2

US-09-936-024-1 (1-271) x US-09-935-727-28 (1-1796)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTRGAGCGCTGCCGC 267

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaPro---------------------- 112
           ||||||||||||||||||||||||||||||||||
Db     388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGG 447

Qy     112 ------------------------------------------------------------ 112

Db     448 GCCCCCAGGAGTGGTGGCCGGAGGTGTGGCAGGGGTCAGGTTGCTGGTCCCAGCCTTGCA 507

Qy     113 ----------------------------------------------------GlyThrPr 115
                                                                   ||||||||
Db     508 CCCTGAGCTAGGACACCAGTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCC 567

Qy     115 oSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSe 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 CAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAG 627

Qy     135 rSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPr 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 CTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCC 687

Qy     155 oGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrAr 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 AGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAG 747

Qy     175 gValPro---------------------------------------------------- 177
           |||||||
Db     748 GGTACCAGGTGAGCCAGAGGCCTGAGGGGGCAGCACACTGCAGGCCAGGCCCACTTGTGC 807

Qy     177 ------------------------------------------------------------ 177

Db     808 CCTCACTCCTGCCCCTGCACGTGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGG 867

Qy     177 ------------------------------------------------------------ 177

Db     868 GGCCACAGTGGATTTGAGGGGTCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCT 927

Qy     177 ------------------------------------------------------------ 177

Db     928 CTCAGGGGTGGCTGAGAATTTGGATCTGAGCCAGGGCACAGCCTCCCCTGGGGAGCTCTG 987

Qy     177 ------------------------------------------------------------ 177

Db     988 GGAAAGTGGGCAGCAATCTCCTAACTGCCCGAGGGGAAGGTGGCTGGCTCCTCTGACACG 1047

Qy     177 ------------------------------------------------------------ 177

Db    1048 GGGAAACCGAGGCCTGATGGTAACTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCT 1107

Qy     177 ------------------------------------------------------------ 177

Db    1108 CTGACATGGGGAAACCGAGGCCCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTG 1167

Qy     177 ------------------------------------------------------------ 177

Db    1168 ACCCCCTTAACATCAAGTCAGGTCCGGTCCATCTGCAGGTCCCAACTCGCCCCTTCCGAT 1227

Qy     177 ------------------------------------------------------------ 177

Db    1228 GGCCCAGGAGCCCCAAGCCCTTGCCTGGGCCCCCTTGCCTCTTGCAGCCAAGGTCCGAGT 1287

Qy     177 ------------------------------------------------------------ 177

Db    1288 GGCCGCTCCTGCCCCCTAGGCCTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCTTC 1347

Qy     177 ------------------------------------------------------------ 177

Db    1348 TCCAGTCCCCATCGTTGCACTGCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTC 1407

Qy     177 ------------------------------------------------------------ 177

Db    1408 TCCTGCAAACCCCCCGAGTGGGGCCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAGTGT 1467

Qy     178 ----------------------------------------------GlyAlaGluGluCysG 183
                                                           ||||||||||||||||
Db    1468 GTGTGGGTGAAATGATCGGACCGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAGTGTG 1527

Qy     183 luArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArgL 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1528 AGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGC 1587

Qy     203 euLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAlaA 223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1588 TGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGG 1647

Qy     223 laLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAspGlyAlaL 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1648 CCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGC 1707

Qy     243 euLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGluArgSerV 263
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1708 TGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCG 1767

Qy     263 alArgGluArgPheLeuProValHis 271
           ||||||||||||||||||||||||||
Db    1768 TCCGTGAGCGCTTCCTCCCTGTGCAC 1793

RESULT 10
US-09-935-727-3
; Sequence 3, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
```

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;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1667
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (73)..(582)
US-09-935-727-3

Alignment Scores:
Pred. No.:              6e-67          Length:         1667
Score:                  982.50         Matches:        179
Percent Similarity:     78.85%         Conservative:   0
Best Local Similarity:  78.85%         Mismatches:     2
Query Match:            65.90%         Indels:         46
DB:                     10             Gaps:           1

US-09-936-024-1 (1-271) x US-09-935-727-3 (1-1667)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     160 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 219

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     220 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 279

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     280 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 339

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     340 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 399

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     400 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 459

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaPro---------------------- 112
           ||||||||||||||||||||||||||||||||||
Db     460 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGG 519

Qy     112 ------------------------------------------------------------ 112

Db     520 GCCCCCAGGAGTGGTGGCCGGAGGTGTGGCAGGGGTCAGGTTGCTGGTCCCAGCCTTGCA 579

Qy     113 ----------------------------------------------------GlyThrPr 115
                                                                 ||||||||
Db     580 CCCTGAGCTAGGACACCAGTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCC 639

Qy     115 oSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSe 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 CAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAG 699

Qy     135 rSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPr 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     700 CTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCC 759

Qy     155 oGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrAr 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 AGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAG 819

Qy     175 gValProGlyAlaGluGlu 181
           ||||||||||   |||
Db     820 GGTACCAGGTGAGCCAGAG 838

RESULT 11
US-09-896-096A-3
; Sequence 3, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/896,096A
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
;   LENGTH: 491
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Unknown organism
;   NAME/KEY: unsure
;   LOCATION: 62, 73, 86, 98
;   OTHER INFORMATION: unknown base
US-09-896-096A-3

Alignment Scores:
Pred. No.:              4.78e-58       Length:         491
Score:                  858.00         Matches:        156
Percent Similarity:     95.71%         Conservative:   0
Best Local Similarity:  95.71%         Mismatches:     6
Query Match:            57.55%         Indels:         1
DB:                     10             Gaps:           0

US-09-936-024-1 (1-271) x US-09-896-096A-3 (1-491)

Qy      35 ArgAspSerProThrThrCysGlyProCysProProArgHisTyrThrGlnPheTrpAsn 54
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3 CGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAAN 62

Qy      55 TyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArg 74
             ||||||   |||||||||   |||||||||   |||||||||||||||||||||||
Db      63 TAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGGGGAGCGTGAGGAGGAGGCACGG 122

Qy      75 AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAla 94
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 GCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCT 182

Qy      95 GlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThr 114
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 GGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACC 242
```

```
Qy    115 ProSerGlnAsnThrGlnCysGln-ProCysProProGlyThrPheSerAlaSerSerSe 134
          ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db    243 CCCAGCCAGAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTC 302

Qy    134 rSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnVa 154
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 CAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGT 362

Qy    154 lProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerTh 174
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 GCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCAC 422

Qy    174 rArgValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGlnAs 194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 CAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGA 482

Qy    194 pIleSer 196
          |||||||
Db    483 CATCTCC 489
```

RESULT 12
US-09-894-924-3
; Sequence 3, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/894,924
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Unknown organism
; NAME/KEY: unsure
; LOCATION: 62, 73, 86, 98
; OTHER INFORMATION: unknown base
US-09-894-924-3

Alignment Scores:

Pred. No.:	4.78e-58	Length:	491
Score:	858.00	Matches:	156
Percent Similarity:	95.71%	Conservative:	0
Best Local Similarity:	95.71%	Mismatches:	6
Query Match:	57.55%	Indels:	1
DB:	10	Gaps:	0

US-09-936-024-1 (1-271) x US-09-894-924-3 (1-491)

```
Qy     35 ArgAspSerProThrThrCysGlyProCysProProArgHisTyrThrGlnPheTrpAsn 54
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 CGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAAN 62

Qy     55 TyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArg 74
             ||||||   |||||||||   |||||||||   |||||||||||||||||||||||
```

```
Db     63 TAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGGGGAGCGTGAGGAGGAGGCACGG 122

Qy     75 AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPheAlaHisAla 94
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 GCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCT 182

Qy     95 GlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThr 114
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 GGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACC 242

Qy    115 ProSerGlnAsnThrGlnCysGln-ProCysProProGlyThrPheSerAlaSerSerSe 134
          ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db    243 CCCAGCCAGAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTC 302

Qy    134 rSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnVa 154
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 CAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGT 362

Qy    154 lProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerTh 174
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 GCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCAC 422

Qy    174 rArgValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGlnAs 194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 CAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGA 482

Qy    194 pIleSer 196
          |||||||
Db    483 CATCTCC 489
```

RESULT 13
US-09-877-156-7
; Sequence 7, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 459
; TYPE: DNA
; ORGANISM: human
US-09-877-156-7

Alignment Scores:

Pred. No.:	8.84e-57	Length:	459
Score:	841.00	Matches:	153
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	56.41%	Indels:	0
DB:	10	Gaps:	0

US-09-936-024-1 (1-271) x US-09-877-156-7 (1-459)

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Qy     56 LeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAla 75
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCT 60

Qy     76 CysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPheAlaHisAlaGly 95
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGT 120

Qy     96 PheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrPro 115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC 180

Qy    116 SerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSer 135
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGC 240

Qy    136 SerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPro 155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCA 300

Qy    156 GlySerSerSerHisAspThrLeuCysThrSerCysThrGlyProLeuSerThrArg 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGG 360

Qy    176 ValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIle 195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATC 420

Qy    196 SerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGlu 208
          ||||||||||||||||||||||||||||||||||||||
Db    421 TCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAG 459

RESULT 14
US-09-062-113-92
; Sequence 92, Application US/09062113
; Patent No. US20020051969A1
;  GENERAL INFORMATION:
;    APPLICANT:  GOTO, Masaaki
;    APPLICANT:  TSUDA, Eisuke
;    APPLICANT:  MOCHIZUKI, Shin'ichi
;    APPLICANT:  YANO, Kazuki
;    APPLICANT:  KOBAYASHI, Fumie
;    APPLICANT:  SHIMA, No. US20020051969A1uyuki
;    APPLICANT:  YASUDA, Hisataka
;    APPLICANT:  NAKAGAWA, No. US20020051969A1uaki
;    APPLICANT:  MORINAGA, Tomonori
;    APPLICANT:  UEDA, Masatsugu
;    APPLICANT:  HIGASHIO, Kanji
;    TITLE OF INVENTION:  No. US20020051969A1el Proteins and Methods for Producing
;    TITLE OF INVENTION:  the Proteins
;    NUMBER OF SEQUENCES:  108
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/062,113
;      FILING DATE:  17-APR-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 54977/1995
;      FILING DATE:  20-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 207508/1995
;      FILING DATE:  21-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP96/00374
;      FILING DATE:  20-FEB-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/915,004
;      FILING DATE:  20-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MOORE, Ronda P.
;      REGISTRATION NUMBER:  44,244
;      REFERENCE/DOCKET NUMBER:  FJN-060DV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  981 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..981
;      OTHER INFORMATION:  /note= "(OCIF-DDD1)".
US-09-062-113-92

Alignment Scores:
Pred. No.:                2.81e-27        Length:          981
Score:                    461.00          Matches:         94
Percent Similarity:       53.17%          Conservative:    57
Best Local Similarity:    33.10%          Mismatches:      101
Query Match:              30.92%          Indels:          32
DB:                       10              Gaps:            7

US-09-936-024-1 (1-271) x US-09-062-113-92 (1-981)

Qy      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
          |||   |||          |||   ||||||       :::|||:::|||   :::||||||
Db     76 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT 135

Qy     25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
          |||||||||:::::::::::   |||                 |||   |||   ||||||
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Qy    125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
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Qy    145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
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RESULT 15
US-09-062-113-83
; Sequence 83, Application US/09062113
; Patent No. US20020051969A1
;  GENERAL INFORMATION:
;    APPLICANT:  GOTO, Masaaki
;    APPLICANT:  TSUDA, Eisuke
;    APPLICANT:  MOCHIZUKI, Shin'ichi
;    APPLICANT:  YANO, Kazuki
;    APPLICANT:  KOBAYASHI, Fumie
;    APPLICANT:  SHIMA, No. US20020051969Aluyuki
;    APPLICANT:  YASUDA, Hisataka
;    APPLICANT:  NAKAGAWA, No. US20020051969Aluaki
;    APPLICANT:  MORINAGA, Tomonori
;    APPLICANT:  UEDA, Masatsugu
;    APPLICANT:  HIGASHIO, Kanji
;    TITLE OF INVENTION:  No. US20020051969Alel Proteins and Methods for Producing
;    TITLE OF INVENTION:  the Proteins
;    NUMBER OF SEQUENCES:  108
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/062,113
;      FILING DATE:  17-APR-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 54977/1995
;      FILING DATE:  20-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 207508/1995
;      FILING DATE:  21-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP96/00374
;      FILING DATE:  20-FEB-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/915,004
;      FILING DATE:  20-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MOORE, Ronda P.
;      REGISTRATION NUMBER:  44,244
;      REFERENCE/DOCKET NUMBER:  FJN-060DV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1206 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  -
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;      OTHER INFORMATION:  /note= "(OCIF-C19S)"
US-09-062-113-83

Alignment Scores:
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Score:                    442.50        Matches:         77
Percent Similarity:       57.75%        Conservative:    31
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US-09-936-024-1 (1-271) x US-09-062-113-83 (1-1206)

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Qy     85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
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Job time : 136 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 12:54:06 ; Search time 2673 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION Sequence 2 from Patent WO0128582.
ACCESSION AX119833
VERSION AX119833.1 GI:14036593
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 813)
AUTHORS Bumol,T.F. and Cohen,F.J.
TITLE Therapeutic applications of flint polypeptides
JOURNAL Patent: WO 0128582-A 2 26-APR-2001;

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           ELI LILLY AND COMPANY (US)
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RESULT 2
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DEFINITION  Sequence 2 from Patent WO0142463.
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VERSION     AX167223.1  GI:14596692
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SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 813)
  AUTHORS   Lu,J. and Witcher,D.R.
  TITLE     Improving stability of flint through o-linked glycosylation
  JOURNAL   Patent: WO 0142463-A 2 14-JUN-2001;
            ELI LILLY AND COMPANY (US)
FEATURES             Location/Qualifiers
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  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
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Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
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Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813


RESULT 3
AX375169
LOCUS       AX375169                 813 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 2 from Patent WO0209668.
ACCESSION   AX375169
VERSION     AX375169.1  GI:19169920
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Micanovic,R. and Witcher,D.R.
  TITLE     Pulmonary administration of flint
  JOURNAL   Patent: WO 0209668-A 2 07-FEB-2002;
            ELI LILLY AND COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .813
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      122 a    298 c    267 g    126 t
ORIGIN

  Query Match           100.0%;  Score 813;  DB 6;  Length 813;
  Best Local Similarity  100.0%;  Pred. No. 7e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Db    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Db    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
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Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
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Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813


RESULT 4
AF134240
LOCUS       AF134240                 903 bp    mRNA    linear   PRI 11-MAY-1999
DEFINITION  Homo sapiens tumor necrosis factor receptor homolog (TR6) mRNA,
            complete cds.
ACCESSION   AF134240
VERSION     AF134240.1  GI:4768938
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   Yu,K.Y., Kwon,B., Ni,J., Zhai,Y., Ebner,R. and Kwon,B.S.
  TITLE     A newly identified member of tumor necrosis factor receptor
            superfamily (TR6) suppresses LIGHT-mediated apoptosis
  JOURNAL   J. Biol. Chem. 274 (20), 13733-13736 (1999)
  MEDLINE   99253915
   PUBMED   10318773
REFERENCE   2  (bases 1 to 903)
  AUTHORS   Kwon,B.S. and Yu,K.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAR-1999) Micro/Immunol, Indiana University, 635
            Barnhill Drive, Indianapolis, IN 46202, USA
FEATURES             Location/Qualifiers
     source          1. .903
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_type="T lymphocyte"
                     /tissue_type="blood"
     gene            1. .903
                     /gene="TR6"
     CDS             1. .903
                     /gene="TR6"
                     /note="similar to DcR3"
                     /codon_start=1
                     /product="tumor necrosis factor receptor homolog"
                     /protein_id="AAD29688.1"
                     /db_xref="GI:4768939"
                     /translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
                     ERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEA
                     RACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA
                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
                     VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      129 a    324 c    305 g    145 t
ORIGIN

  Query Match           100.0%;  Score 813;  DB 9;  Length 903;
  Best Local Similarity  100.0%;  Pred. No. 6.8e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db     88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147
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Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db     328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Db     508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Db     628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
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Db     688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
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Db     808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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Db     868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900
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RESULT 5
AF217794
LOCUS       AF217794                1048 bp    mRNA    linear   PRI 12-FEB-2000
DEFINITION  Homo sapiens M68E mRNA, alternatively spliced, complete cds.
ACCESSION   AF217794
VERSION     AF217794.1  GI:6969262
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1048)
  AUTHORS   Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
            Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
            Caskey,C.T.
  TITLE     Overexpression of M68/DcR3 in human gastrointestinal tract tumors
            independent of gene amplification and its location in a four-gene
            cluster
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
  MEDLINE   20122600
   PUBMED   10655513
REFERENCE   2  (bases 1 to 1048)
  AUTHORS   Bai,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,
            Sumneytown Pike, West Point, PA 19403, USA
FEATURES             Location/Qualifiers
     source          1. .1048
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                     /chromosome="20"
                     /map="20q13.3"
                     /cell_type="adenocarcinoma"
                     /tissue_type="pancreas"
     CDS             53. .955
                     /note="TNFR; decoy receptor; DCR3; alternatively spliced"
                     /codon_start=1
                     /product="M68E"
                     /protein_id="AAF33686.1"
                     /db_xref="GI:6969263"
                     /translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
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                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
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BASE COUNT      160 a    367 c    335 g    186 t
ORIGIN

  Query Match           100.0%;  Score 813;  DB 9;  Length 1048;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db     140 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 199

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 259

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     260 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 319

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db     320 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 379

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db     380 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 439

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db     440 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 499

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Db     500 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 559

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Db     560 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 619

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
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Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
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Db    740 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 799

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    800 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 859

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
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Db    860 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 919

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||
Db    920 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 952


RESULT 6
AX082868
LOCUS       AX082868               1055 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 1 from Patent WO0110908.
ACCESSION   AX082868
VERSION     AX082868.1  GI:13184802
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1055)
  AUTHORS   Hsu,H.
  TITLE     Ntr3, a member of the tnf-receptor supergene family
  JOURNAL   Patent: WO 0110908-A 1 15-FEB-2001;
            Amgen Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1055
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     CDS             67. .969
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                     /codon_start=1
                     /protein_id="CAC33261.1"
                     /db_xref="GI:13184803"
                     /translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
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BASE COUNT      160 a    369 c    340 g    186 t
ORIGIN

  Query Match           100.0%;  Score 813;  DB 6;  Length 1055;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db    154 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 213

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db    214 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 273

Qy    121 TGTGGCCCGTGTCCACCGCGCCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Db    274 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 333

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 393

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db    394 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 453

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 513

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Db    514 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 573

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Db    574 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 633

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 693

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Db    694 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 753

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
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Db    754 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 813

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
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Db    814 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 873

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 933

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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Db    934 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 966


RESULT 7
AX055373
LOCUS       AX055373               1114 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 3 from Patent WO0073452.
ACCESSION   AX055373
VERSION     AX055373.1  GI:12228659
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1114)
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
            Tumas,D., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 0073452-A 3 07-DEC-2000;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1114
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      188 a    379 c    356 g    191 t
ORIGIN

  Query Match           100.0%;  Score 813;  DB 6;  Length 1114;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db     248 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 307

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Db     308 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db     368 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 427

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db     428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db     488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Db     608 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 667

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
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Db     668 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 727

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Db     728 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 787

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
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Db     788 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 847

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
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Db     848 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 907

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Db     908 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 967

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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Db     968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000
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RESULT 8
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LOCUS       AX056645               1114 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 1 from Patent WO0075316.
ACCESSION   AX056645
VERSION     AX056645.1  GI:12309639
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1114)
  AUTHORS   Ashkenazi,A.J., Goddard,A., Gurney,A.L., Hillan,K., Napier,M. and
            Wood,W.I.
  TITLE     Methods and compositions for inhibiting neoplastic cell growth
  JOURNAL   Patent: WO 0075316-A 1 14-DEC-2000;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1114
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      188 a    379 c    356 g    191 t
ORIGIN
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  Query Match           100.0%;  Score 813;  DB 6;  Length 1114;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db     188 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 247

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db     248 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 307

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Db     308 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db     428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db     488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Db     548 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 607

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
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Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Db     728 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 787

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     788 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 847

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
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Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
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Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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Db     968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000
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RESULT 9
AF104419
LOCUS       AF104419               1114 bp    mRNA    linear   PRI 06-JAN-1999
DEFINITION  Homo sapiens decoy receptor 3 (DcR3) mRNA, complete cds.
ACCESSION   AF104419
VERSION     AF104419.1  GI:4106877
KEYWORDS    .
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SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1114)
  AUTHORS   Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
            Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
            Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
            Goddard,A.D., Botstein,D. and Ashkenazi,A.
  TITLE     Genomic amplification of a decoy receptor for Fas ligand in lung
            and colon cancer
  JOURNAL   Nature 396 (6712), 699-703 (1998)
  MEDLINE   99087326
   PUBMED   9872321
REFERENCE   2  (bases 1 to 1114)
  AUTHORS   Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
            Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
            Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
            Goddard,A.D., Botstein,D. and Ashkenazi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way,
            San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1114
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                     activity"
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                     factor receptor family; amplified in lung and colon
                     cancer"
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                     /db_xref="GI:4106878"
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                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      188 a    379 c    356 g    191 t
ORIGIN

  Query Match           100.0%;  Score 813;  DB 9;  Length 1114;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db     188 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 247

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db     248 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 307

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db     368 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 427

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db     428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db     488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Db     548 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 607

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Db     608 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 667

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     668 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 727

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
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Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
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Db     908 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 967

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db     968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000


RESULT 10
BC017065
LOCUS       BC017065                1125 bp    mRNA    linear   PRI 09-NOV-2001
DEFINITION  Homo sapiens, tumor necrosis factor receptor superfamily, member
            6b, decoy, clone MGC:9587 IMAGE:3886635, mRNA, complete cds.
ACCESSION   BC017065
VERSION     BC017065.1  GI:16877637
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1125)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
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           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           Series: IRAK Plate: 22 Row: d Column: 23
           This clone was selected for full length sequencing because it
           passed the following selection criteria: matched mRNA gi: 14790166.
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                     undifferentiated."
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BASE COUNT      200 a    378 c    356 g    191 t
ORIGIN

  Query Match             100.0%;  Score 813;  DB 9;  Length 1125;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 246

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 306

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 366

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 426

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 486

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 546

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 606

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 666

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 726

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 786

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 846

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 906

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 966

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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Db     967 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 999


RESULT 11
AX017828
LOCUS       AX017828               1168 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9946376.
ACCESSION   AX017828
VERSION     AX017828.1  GI:10042431
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1168)
  AUTHORS   Kroeger,B.
  TITLE     Receptor from the superfamily of tnt-receptors from the human lung
  JOURNAL   Patent: WO 9946376-A 1 16-SEP-1999;
            BASF AG (DE); KROEGER BURKHARD (DE)
FEATURES             Location/Qualifiers
     source          1. .1168
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                     /db_xref="taxon:9606"
     CDS             134. .1036
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC07698.1"
                     /db_xref="GI:10042432"
                     /translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
                     ERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEA
                     RACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA
                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
                     VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      194 a    392 c    371 g    211 t
ORIGIN

  Query Match             100.0%;  Score 813;  DB 6;  Length 1168;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 280

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     281 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 340

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     341 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 400

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     401 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 460

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db    461 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 520

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Db    521 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 580

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Db    581 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 640

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Db    641 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 700

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Db    701 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 760

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Db    761 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 820

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Db    821 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 880

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Db    881 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 940

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Db    941 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 1000

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813

Db   1001 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1033


RESULT 12
AR171895
LOCUS       AR171895               1347 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 18 from patent US 6297367.
ACCESSION   AR171895
VERSION     AR171895.1  GI:17910845
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1347)
  AUTHORS   Tribouley,C.
  TITLE     Polynucleotide encoding TNFL1
  JOURNAL   Patent: US 6297367-A 18 02-OCT-2001;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      230 a    444 c    443 g    230 t
ORIGIN

  Query Match           100.0%;  Score 813;  DB 6;  Length 1347;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Db    405 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 464

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Db    465 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 524

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Db    525 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 584

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Db    585 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 644

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Db    645 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 704

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Db    705 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 764

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Db    765 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 824

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Db    825 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 884

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Db    885 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 944

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Db    945 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 1004

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Db   1005 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 1064

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Db   1065 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 1124

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Db   1125 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 1184

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813

Db   1185 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1217


RESULT 13
AF217793
LOCUS       AF217793               1428 bp    mRNA    linear   PRI 12-FEB-2000
DEFINITION  Homo sapiens M68C mRNA, alternatively spliced, complete cds.
ACCESSION   AF217793
VERSION     AF217793.1  GI:6969260
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1428)
  AUTHORS   Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
            Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
            Caskey,C.T.
  TITLE     Overexpression of M68/DcR3 in human gastrointestinal tract tumors
            independent of gene amplification and its location in a four-gene
            cluster
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
  MEDLINE   20122600
   PUBMED   10655513
REFERENCE   2  (bases 1 to 1428)
  AUTHORS   Bai,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,
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          Sumneytown Pike, West Point, PA 19403, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /map="20q13.3"
                     /cell_type="germ cell tumor"
     CDS             435. .1337
                     /note="TNFR; decoy receptor; DCR3; alternatively spliced"
                     /codon_start=1
                     /product="M68C"
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                     /db_xref="GI:6969261"
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                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
                     VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      240 a    500 c    448 g    240 t
ORIGIN

  Query Match           100.0%;  Score 813;  DB 9;  Length 1428;
  Best Local Similarity  100.0%;  Pred. No. 6.2e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    522 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 581

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db    582 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 641

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Db    642 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 701

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db    702 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 761

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    762 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 821

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    822 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 881

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    882 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 941

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Db    942 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 1001

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1002 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 1061

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Db   1062 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 1121

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
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Db   1122 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 1181

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1182 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 1241

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
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Db   1242 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 1301

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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Db   1302 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1334


RESULT 14
AB029011
LOCUS       AB029011               4945 bp    mRNA    linear   PRI 10-MAY-2002
DEFINITION  Homo sapiens mRNA for KIAA1088 protein, partial cds.
ACCESSION   AB029011
VERSION     AB029011.2  GI:20521759
KEYWORDS    .
SOURCE      Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
            clone:hk02589s1.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kikuno,R., Nagase,T., Ishikawa,K., Hirosawa,M., Miyajima,N.,
            Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XIV. The complete sequences of 100 new cDNA clones from brain which
            code for large proteins in vitro
  JOURNAL   DNA Res. 6 (3), 197-205 (1999)
  MEDLINE   99397452
   PUBMED   10470851
REFERENCE   2  (bases 1 to 4945)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute,
            Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
COMMENT     On May 9, 2002 this sequence version replaced gi:5689512.
FEATURES             Location/Qualifiers
     source          1. .4945
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                     /clone="hk02589s1"
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                     /clone_lib="pBluescriptII SK plus"
                     /note="This sequence was obtained by subcloning of the DNA
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                     derived from a RT-PCR product (Brain) and 835 - 4945 was
                     derived from hk02589)."
     gene            1. .4945
                     /gene="KIAA1088"
     CDS             <1. .4203
                     /gene="KIAA1088"
                     /codon_start=1
                     /product="KIAA1088 protein"
                     /protein_id="BAA83040.2"
                     /db_xref="GI:20521760"
                     /translation="MPKIVLNGVTVDFPFQPYKCQQEYMTKVLECLQQKVNGILESPT
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                     HLCRKKVASRSCHFYNNVEEKSLEQELASPILDIEDLVKSGSKHRVCPYYLSRNLKQQ
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                     KVLSYWCFSPGHSMHELVRQGVRSLILTSGTLAPVSSFALEMQIPFPVCLENPHIIDK
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                     EKSLEFWRARDLARKMEALKPLFVEPRSKGSFSETISAYYARVAAPGSTGATFLAVCR
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                     GRGCGYRPEHSIPRRQRAQPVLDPTGRTAPDPKLTVSTAAAQQLDPQEHLNQGRPHLS
                     PRPPPTGDPGSHPQWGSGVPRAGKQGQHAVSAYLADARRALGSAGCSQLLAALTAYKQ
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BASE COUNT      963 a   1581 c   1529 g    872 t
ORIGIN

  Query Match           100.0%;  Score 813;  DB 9;  Length 4945;
  Best Local Similarity  100.0%;  Pred. No. 4.9e-125;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db   3995 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 4054

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db   4055 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 4114

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Db   4115 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 4174

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db   4175 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 4234

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4235 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 4294

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db   4295 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 4354

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Db   4355 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 4414

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
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Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
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Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
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Db   4655 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 4714

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
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Db   4715 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 4774

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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RESULT 15
BC034349
LOCUS       BC034349                1150 bp    mRNA    linear   PRI 08-JUL-2002
DEFINITION  Homo sapiens, tumor necrosis factor receptor superfamily, member
            6b, decoy, clone MGC:21079 IMAGE:4752507, mRNA, complete cds.
ACCESSION   BC034349
VERSION     BC034349.1  GI:21706464
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
            Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
            Richards, S., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 28 Row: o Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 14790166.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="MGC:21079 IMAGE:4752507"
                     /tissue_type="Skin, squamous cell carcinoma"
                     /clone_lib="NCI_CGAP_Skn4"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6.ccdb"
     CDS             109. .1011
                     /codon_start=1
                     /product="tumor necrosis factor receptor superfamily,
                     member 6b, decoy"
                     /protein_id="AAH34349.1"
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                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
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BASE COUNT      222 a    382 c    348 g    198 t
ORIGIN

  Query Match           99.8%;  Score 811.4;  DB 9;  Length 1150;
  Best Local Similarity  99.9%;  Pred. No. 1.2e-124;
  Matches  812;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db    196 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 255

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    256 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 315

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db    376 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 435

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db    436 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 495

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Db    556 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 615

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Db    616 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 675

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 735

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
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Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
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Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    916 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 975

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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Db    976 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1008
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Search completed: January 6, 2003, 14:40:26
Job time : 2682 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 12:53:01 ; Search time 230 Seconds
(without alignments)
7960.324 Million cell updates/sec

Title: US-09-936-024-2
Perfect score: 813
Sequence: 1 gtggcagaaacacccaccta.....agcgcttcctccctgtgcac 813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	813	100.0	813	20	AAZ25377	Human mFLINT #1 nu
2	813	100.0	813	21	AAA75999	DNA encoding a mat
3	813	100.0	813	21	AAA88730	Human FAS ligand i
4	813	100.0	813	21	AAA51077	Mature human FLINT
5	813	100.0	813	22	AAD07380	Human mature fas l
6	813	100.0	813	24	AAD27868	Human mature FLINT
7	813	100.0	900	20	AAZ25375	Human FLINT #1 nuc
8	813	100.0	900	21	AAA53208	Human Fas ligand i
9	813	100.0	900	21	AAA51075	Human FLINT coding
10	813	100.0	903	20	AAX22300	Orphan receptor (H
11	813	100.0	1055	22	AAF62705	Human NTR3 nucleot
12	813	100.0	1066	21	AAA53802	M68 TNF receptor r
13	813	100.0	1077	19	AAV39085	Human tumour necro
14	813	100.0	1077	21	AAA37772	Human tumour necro
15	813	100.0	1077	24	AAD33281	Human tumour necro
16	813	100.0	1114	20	AAX32744	Human DcR3 polypep
17	813	100.0	1114	21	AAC58367	Human PRO212 nucle
18	813	100.0	1114	21	AAC58581	Human PRO212 prote
19	813	100.0	1114	21	AAA77537	Human PRO212 cDNA
20	813	100.0	1114	22	AAC84421	Human PRO212 polyp
21	813	100.0	1114	22	AAC91462	Human PRO212 cDNA.
22	813	100.0	1164	19	AAV07654	Nucleotide sequenc
23	813	100.0	1168	20	AAZ09998	Human lung TNF-rec
24	813	100.0	1179	22	AAH33171	Human colon cancer
25	813	100.0	1205	20	AAX07226	Human tumour necro
26	813	100.0	1347	21	AAC63764	Human soluble TNF
27	813	100.0	1428	21	AAA53801	M68 TNF receptor r
28	813	100.0	1462	20	AAX76052	Mammalian tumour n
29	811.4	99.8	825	20	AAZ25378	Human mFLINT #2 nu
30	811.4	99.8	825	21	AAA51078	Human mature FLINT
31	811.4	99.8	936	20	AAZ25376	Human FLINT #2 nuc
32	809.8	99.6	936	21	AAA88731	Human FAS ligand i
33	809.8	99.6	936	21	AAA51076	Human FLINT coding
34	809.8	99.6	936	22	AAD07385	Human fas ligand i
35	809.8	99.6	936	22	AAF89920	Nucleotide sequenc
36	809.8	99.6	936	22	AAF84738	Nucleotide sequenc
37	809.8	99.6	936	22	AAF84739	Nucleotide sequenc
38	809.8	99.6	936	22	AAF77696	Human FLINT native
39	809.8	99.6	936	24	AAD27869	Human FLINT analog
40	809.8	99.6	1137	21	AAZ92404	cDNA encoding huma
41	798.6	98.2	1224	24	ABQ55057	Human ovarian anti
42	728.2	89.6	900	21	AAA53209	Monkey Fas ligand
43	647	79.6	767	20	AAX23419	Human APO6 DNA. H
44	644.2	79.2	899	20	AAX89503	DNA encoding a hum
45	533.4	65.6	1859	21	AAC63765	Human soluble TNF

ALIGNMENTS

RESULT 1
AAZ25377
ID AAZ25377 standard; cDNA; 813 BP.
XX
AC AAZ25377;
XX
DT 17-DEC-1999 (first entry)
XX
DE Human mFLINT #1 nucleotide sequence.
XX
KW Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancytopenic condition;
KW myocardial ischaemia; ss.
XX
OS Homo sapiens.
XX
PN WO9950413-A2.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US06797.
XX
PR 30-MAR-1998; 98US-0079856.
PR 20-MAY-1998; 98US-0086074.
PR 09-SEP-1998; 98US-0099643.
PR 17-DEC-1998; 98US-0112577.
PR 18-DEC-1998; 98US-0112703.
PR 18-DEC-1998; 98US-0112933.
PR 22-DEC-1998; 98US-0113407.

XX
PA (ELIL) LILLY & CO ELI.
XX
PI Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
PI Hui KY, Kharitonenkov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
PI Song HY, Wang J, Wu X, Zuckerman SH;
XX
DR WPI; 1999-591319/50.
DR P-PSDB; AAZ42184.
XX
PT Use of mature FLINT for treating acute liver failure, inflammation,
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
PT and proinflammatory activity
XX
PS Claim 29; Fig 3; 99pp; English.
XX
CC The present invention describes therapeutic applications of mature FLINT
CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC (mFLINT), which is a member of the tumour necrosis factor receptor
CC superfamily, is used for treating acute liver failure, inflammation of
CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC injury or disorder such as hypercoagulation (including use with
CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC or disorder, Type I diabetes, cancer, cell damage or damage to an
CC innocent bystander tissue that is induced by a chemotherapeutic agent or
CC therapeutic irradiation, treating haematopoietic progenitor cells that
CC have been exposed to therapeutic radiation or chemotherapy, aplastic
CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC also used for promoting the growth or differentiation of a haematopoietic
CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC resulting from abnormal myocardial ischaemia. The present sequence
CC encodes human mFLINT.
XX
SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match 100.0%; Score 813; DB 20; Length 813;
Best Local Similarity 100.0%; Pred. No. 5.1e-145;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
```

RESULT 2
AAA75999
ID AAA75999 standard; DNA; 813 BP.
XX
AC AAA75999;
XX
DT 19-FEB-2001 (first entry)
XX
DE DNA encoding a mature human FAS Ligand Inhibitory Protein (FLINT).
XX
KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW acute respiratory distress syndrome; ulcerative colitis;
KW chronic obstructive pulmonary disease; Crohn's disease; ss.
XX
OS Homo sapiens.
XX
PN WO200058465-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000WO-US06417.
XX
PR 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140077.
PR 21-JUN-1999; 99US-0140156.
PR 20-OCT-1999; 99US-0160566.
PR 18-FEB-2000; 2000US-0183398.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;
PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;
PI Wroblewski VJ;
XX
DR WPI; 2000-656167/63.
DR P-PSDB; AAB19334.
XX
PT FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT disease -
XX
PS Claim 37; Page 113; 114pp; English.
XX
CC The present sequence encodes a mature human FAS Ligand Inhibitory
CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC FLINT protein is modified to produce analogues, which have greater

```
CC   potency, longer in vivo half-lives, decreased aggregation, decreased
CC   absorption onto surfaces, increased solubility and improved ease of
CC   formulation. The FLINT analogue is useful for treating a patient
CC   suffering from disease or condition relating to abnormal apoptosis such
CC   as acute lung injury, acute respiratory distress syndrome, pulmonary
CC   fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC   Crohn's disease.
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

  Query Match             100.0%;  Score 813;  DB 21;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813


RESULT 3
AAA88730
ID   AAA88730 standard; cDNA; 813 BP.
XX
AC   AAA88730;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Human FAS ligand inhibitor protein FLINT cDNA.
XX
KW   FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW   acute lung injury; acute respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   ulcerative colitis; therapy; organ transpantation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058466-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06418.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140073.
PR   04-AUG-1999;   99US-0147071.
PR   20-OCT-1999;   99US-0160524.
PR   21-OCT-1999;   99US-0160669.
PR   20-DEC-1999;   99US-0172744.
PR   26-JAN-2000; 2000US-0178184.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Rathnachalam R,  Witcher DR;
XX
DR   WPI; 2000-664925/64.
DR   P-PSDB; AAB19705.
XX
PT   Novel protease resistant FAS ligand inhibitory protein analogues
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases -
XX
PS   Disclosure; Page 95; 100pp; English.
XX
CC   The present sequence is that of cDNA coding for human FAS ligand
CC   inhibitory protein FLINT mature protein (see AAB19705).  FLINT is a
CC   tumour necrosis factor receptor homologue that binds FAS ligand,
CC   preventing its interaction with FAS.  This interaction is implicated
CC   in runaway apoptosis and inflammatory disease.  FLINT also binds to
CC   LIGHT, a membrane-bound ligand, which may play a role in immune
CC   modulation and apoptosis.  The invention relates to novel FLINT
CC   analogues (see also AAB19706-09) that are resistant to proteolysis
CC   by trypsin-like proteases between positions 218 and 219 of the
CC   FLINT mature protein sequence.  Nucleic acids, vectors and
CC   transformed host cells for recombinant production of the analogues
CC   are claimed.  FLINT cDNA is used as a template for introducing the
CC   required point mutations e.g. via PCR mutagenesis.  The protease
CC   resistant FLINT analogues are used to prevent or treat acute lung
CC   injury, acute respiratory stress syndrome, ulcerative colitis,
CC   chronic obstructive pulmonary disease, pulmonary fibrosis, to
CC   inhibit T lymphocyte activation, and to facilitate organ
CC   preservation for transplantation (claimed).
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

  Query Match             100.0%;  Score 813;  DB 21;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
```

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RESULT 4
AAA51077
ID   AAA51077 standard; DNA; 813 BP.
XX
AC   AAA51077;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Mature human FLINT coding sequence.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     1..813
FT                   /*tag=  a
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   P-PSDB; AAY96598.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 8; Fig 3A-B; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
```

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  Query Match           100.0%;  Score 813;  DB 21;  Length 813;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813


RESULT 5
AAD07380
ID   AAD07380 standard; cDNA; 813 BP.
XX
AC   AAD07380;
XX
DT   04-AUG-2001  (first entry)
XX
DE   Human mature fas ligand inhibitory protein (FLINT) cDNA.
XX
KW   Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
KW   TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KW   acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KW   chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
KW   rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
KW   fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KW   chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KW   vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KW   insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KW   Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KW   Down's syndrome; multiple sclerosis; cytostatic; nootropic;
KW   neuroprotective; vasotropic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..813
FT                   /*tag=  a
FT                   /product= "Human mature fas ligand inhibitory protein
FT                   (FLINT)"
FT                   /note= "CDS does not include start and stop codon"
FT                   /partial
XX
PN   WO200142463-A1.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US30166.
XX
PR   07-DEC-1999;   99US-0169367.
PR   07-DEC-1999;   99US-0169381.
PR   07-DEC-1999;   99US-0169412.
PR   23-MAR-2000; 2000US-0191430.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Lu J,  Witcher DR;
XX
DR   WPI; 2001-381684/40.
DR   P-PSDB; AAE03567.
XX
PT   New FLINT polypeptide for treating and/or preventing acute lung injury,
PT   acute respiratory distress syndrome, ulcerative colitis, and
PT   graft-versus-host disease, comprises O-linked or N-linked
PT   oligosaccharides -
XX
PS   Example 1; Page 53; 60pp; English.
XX
CC   The present sequence is human mature fas ligand inhibitory protein
CC   (FLINT) cDNA. FLINT, a homologue of tumour necrosis factor receptor
CC   protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC   interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC   oligosaccharides is useful for preventing or treating acute lung injury
CC   (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC   chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC   to facilitate organ preservation for transplantation and to inhibit T
CC   lymphocyte activation. FLINT is useful for treating and/or preventing
CC   diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC   fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC   (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC   host disease, cutaneous inflammation, vascular leak syndrome,
CC   Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC   diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC   Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC   psoriasis, Down's syndrome, and multiple sclerosis.
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

  Query Match             100.0%;  Score 813;  DB 22;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
                ||||||||||||||||||||||||||||||||
Db     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813


RESULT 6
AAD27868
ID   AAD27868 standard; DNA; 813 BP.
XX
AC   AAD27868;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human mature FLINT DNA.
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..813
FT                   /*tag=  a
FT                   /product= "Mature FLINT protein"
FT                   /note= "Does not include start and stop codons"
FT                   /partial
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
DR   P-PSDB; AAE14578.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page 30; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analog.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   mature FLINT DNA.
XX
SQ   Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

  Query Match             100.0%;  Score 813;  DB 24;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
                ||||||||||||||||||||||||||||||||
Db     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813


RESULT 7
AAZ25375
```

```
ID   AAZ25375 standard; cDNA; 900 BP.
XX
AC   AAZ25375;
XX
DT   17-DEC-1999  (first entry)
XX
DE   Human FLINT #1 nucleotide sequence.
XX
KW   Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW   apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW   sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW   reperfusion-associated injury; aplastic anaemia; differentiation;
KW   growth; myelodysplastic syndrome; pancytopenic condition;
KW   myocardial ischaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950413-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06797.
XX
PR   30-MAR-1998;   98US-0079856.
PR   20-MAY-1998;   98US-0086074.
PR   09-SEP-1998;   98US-0099643.
PR   17-DEC-1998;   98US-0112577.
PR   18-DEC-1998;   98US-0112703.
PR   18-DEC-1998;   98US-0112933.
PR   22-DEC-1998;   98US-0113407.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bumol TF,  Dou S,  Glasebrook AL,  Gould KE,  Hale JE,  Heuer JG;
PI   Hui KY,  Kharitonenkov A,  Mizrahi J,  Na S,  Noblitt TW,  Reidy CA;
PI   Song HY,  Wang J,  Wu X,  Zuckerman SH;
XX
DR   WPI; 1999-591319/50.
DR   P-PSDB; AAY42182.
XX
PT   Use of mature FLINT for treating acute liver failure, inflammation,
PT   cancer, and diabetes  - by prevention of FasL-Fas mediated apoptotic
PT   and proinflammatory activity
XX
PS   Claim 28; Fig 1; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   encodes human FLINT.
XX
SQ   Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

  Query Match           100.0%;  Score 813;  DB 20;  Length 900;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
           |||||||||||||||||||||||||||||||
Db     868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900


RESULT 8
AAA53208
ID   AAA53208 standard; cDNA; 900 BP.
XX
AC   AAA53208;
XX
DT   03-JAN-2001  (first entry)
XX
DE   Human Fas ligand inhibitor FLINT coding sequence.
XX
KW   Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
KW   inflammation; infectious disease; ischaemia; Alzheimer's disease;
KW   Parkinson's disease; Crohn's disease; transplantation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..900
FT                   /*tag=  a
```

```
FT                   /product= "FLINT"
FT                   /partial
FT   sig_peptide     1..90
FT                   /*tag=  b
FT   mat_peptide     91..900
FT                   /*tag=  c
XX
PN   WO200034782-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-US28696.
XX
PR   09-DEC-1998;   98US-0111575.
PR   09-DEC-1998;   98US-0111580.
PR   07-JAN-1999;   99US-0115069.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Rosteck PRJ,  Song HY,  Su EW;
XX
DR   WPI; 2000-431379/37.
DR   P-PSDB; AAB03621.
XX
PT   Novel monkey Fas ligand inhibitor polypeptides, useful for treating
PT   inflammatory or autoimmune disease such as rheumatoid arthritis,
PT   infectious diseases such as chronic hepatitis, and
PT   Ischaemia/Re-perfusion conditions -
XX
PS   Example 1; Page 88-91; 101pp; English.
XX
CC   The present sequence is the coding sequence of the human Fas ligand
CC   inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC   apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC   such as rheumatoid arthritis, inflammatory bowel disease,
CC   graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC   infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC   hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC   ulceration, ischaemia and reperfusion conditions including acute
CC   myocardial infarction, acute coronary syndrome, congestive heart failure
CC   and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung
CC   injury and acute respiratory distress syndrome, Crohn's disease, brain
CC   trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic
CC   anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
CC   multiple sclerosis. In addition, the gene and protein can be used to
CC   prevent apoptosis following organ transplantation.
XX
SQ   Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
```

```
  Query Match             100.0%;  Score 813;  DB 21;  Length 900;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db     868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900
```

```
RESULT 9
AAA51075
ID   AAA51075 standard; DNA; 900 BP.
XX
AC   AAA51075;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human FLINT coding sequence.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..900
FT                   /*tag=  a
FT                   /product= FLINT
FT                   /partial
FT   sig_peptide     1..87
FT                   /*tag=  b
FT   mat_peptide     88..900
FT                   /*tag=  c
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
```

```
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   P-PSDB; AAY96596.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 7; Fig 1A-B; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

  Query Match             100.0%;  Score 813;  DB 21;  Length 900;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900


RESULT 10
AAX22300
ID   AAX22300 standard; DNA; 903 BP.
XX
AC   AAX22300;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.
XX
KW   HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
KW   tumour necrosis factor receptor; muscle disorder; bone mass; screening;
KW   muscle metabolism; binding agent; cognate ligand; ss.
XX
OS   Homo sapiens.
XX
PN   WO9907738-A2.
XX
PD   18-FEB-1999.
XX
PF   04-AUG-1998;   98WO-US16202.
XX
PR   06-AUG-1997;   97US-0054869.
XX
PA   (PROC ) PROCTER & GAMBLE CO.
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Masiakowski PJ,  Morris J,  Valenzuela DM;
XX
DR   WPI; 1999-167365/14.
DR   P-PSDB; AAW95082.
XX
PT   Novel orphan human receptor polypeptide and nucleic acid - useful as
PT   diagnostic reagents and for treatment of muscle disorders
XX
PS   Claim 2; Page 21; 23pp; English.
XX
CC   This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The
CC   protein is related to osteoprotegerin (OPG) and to tumour necrosis factor
CC   receptor (TNFR). Host cells transformed with a vector comprising the
CC   HUMAN NTR-1 nucleic acid are used for the recombinant expression of the
CC   protein. HUMAN NTR-1 proteins and antibodies immuno specific for the
CC   protein are useful for diagnosis and treatment of humans and animals,
CC   especially muscle disorders, as the receptor is involved in regulation of
CC   bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful
CC   for screening for novel binding agents, and cognate ligands, which may be
CC   used to treat disorders associated with HUMAN NTR-1 imbalance.
XX
SQ   Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;

  Query Match             100.0%;  Score 813;  DB 20;  Length 903;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900
```

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RESULT 11
AAF62705
ID   AAF62705 standard; cDNA; 1055 BP.
XX
AC   AAF62705;
XX
DT   02-MAY-2001  (first entry)
XX
DE   Human NTR3 nucleotide sequence.
XX
KW   Human; NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;
KW   antianaemic; immunosuppressive; antidiabetic; antiviral; antibacterial;
KW   cytostatic; neuroprotective; antiinflammatory; anorectic; vasotropic;
KW   antirheumatoid; antiarthritic; cerebroprotective; tuberculostatic;
KW   gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;
KW   infection; ss.
XX
OS   Homo sapiens.
XX
PN   WO200110908-A1.
XX
PD   15-FEB-2001.
XX
PF   02-AUG-2000; 2000WO-US21287.
XX
PR   04-AUG-1999;   99US-0147297.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Hsu H;
XX
DR   WPI; 2001-191521/19.
DR   P-PSDB; AAB71754.
XX
PT   New tumor necrosis factor receptor, NTR3, useful for treating cancers,
PT   stroke, anemia, obesity, rheumatoid arthritis and transplantation
PT   rejection -
XX
PS   Claim 1; Page 128-129; 135pp; English.
XX
CC   The present sequence encodes the tumour necrosis factor (TNF) receptor
CC   polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful
CC   for treating diseases such as acquired-immunodeficiency syndrome (AIDS),
CC   anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,
CC   diabetes mellitus, disseminated intravascular coagulopathy, erythroid
CC   sick syndrome, haemorrhagic shock, hepatitis, insulin resistance,
CC   leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,
CC   obesity, rejection of transplanted organs, rheumatoid arthritis, septic
CC   shock syndrome, stroke, adult respiratory distress syndrome (ARDS),
CC   tuberculosis, and a number of viral diseases. The NTR3 polypeptide is
CC   useful for identifying or developing new (ant)agonists of NTR3. It may
CC   be used as an immunogen to which antibodies may be raised. NTR3 nucleic
CC   acid molecules may be useful as hybridisation probes in diagnostic assays
CC   to test, either qualitatively or quantitatively, for the presence of an
CC   NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid
CC   samples.
XX
SQ   Sequence 1055 BP; 160 A; 369 C; 340 G; 186 T; 0 other;
```

```
  Query Match           100.0%;  Score 813;  DB 22;  Length 1055;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 213

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 273

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 333

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 393

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 453

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 513

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    514 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 573

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 633

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 693

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 753

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 813

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 873

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 933

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    934 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 966
```

```
RESULT 12
AAA53802
ID   AAA53802 standard; cDNA; 1066 BP.
XX
AC   AAA53802;
XX
DT   19-DEC-2000  (first entry)
XX
DE   M68 TNF receptor related protein coding sequence.
XX
KW   M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
KW   receptor; immune response; cell differentiation; ligand; cancer;
KW   bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
KW   Grave's disease; idiopathic myxodema; autoimmune diabetes;
KW   thrombotic thrombocytopenic purpura; multiple sclerosis;
KW   liver diseases; autoimmune gastritis; ulcerative colitis;
KW   glomerulonephritis; pulmonary fibrosis; heart failure;
KW   atherosclerosis; aplastic anaemia; myelodisplastic syndromes;
KW   osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
KW   myocardial infarction; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53..955
FT                   /*tag=  a
FT                   /product= M68 polypeptide
XX
PN   WO200046247-A1.
XX
PD   10-AUG-2000.
XX
PF   04-FEB-2000; 2000WO-US03037.
XX
PR   05-FEB-1999;   99US-0118902.
PR   20-DEC-1999;   99US-0172754.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Bai C;
XX
DR   WPI; 2000-506066/45.
DR   P-PSDB; AAY97246.
XX
PT   Isolated human M68 nucleic acids and proteins which are part of the
PT   tumor necrosis factor receptor (TNFR) family, useful for identifying
PT   modulators that may be used to treat various diseases e.g. cancer,
PT   osteoporosis, Alzheimer's disease
XX
PS   Claim 21; Page 73-75; 80pp; English.
XX
CC   The M68 protein is a member of a family of proteins which have
CC   roles in immune responses, cell death, cell proliferation and
CC   stimulation of cell differentiation. M68 lacks a transmembrane domain
CC   and is a secreted factor suggesting that it functions as a natural
CC   inhibitor for its ligand. The altered expression pattern of M68 in a
CC   multitude of tissues suggests that M68 may play a role in cancer by
CC   binding to its ligand and blocking apoptotic cell death induced by
CC   such a ligand. This anti-apoptopic role of M68 suggests that
CC   modulators of M68 will be useful in treatment of apoptosis-related
CC   diseases such as various forms of cancer and various bone disorders.
CC   M68 nucleic acids and proteins are therefore useful for treating
CC   conditions involving atypical apoptosis and for identifying
CC   modulators of M68. Modulators of M68 are useful for treatment of
CC   cancer and other diseases associated with abnormal levels of
CC   apoptosis including systemic lupus erythematosus, Hashimoto's
CC   thyroiditis, Grave's disease, idiopathic myxodema, autoimmune
CC   diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
CC   liver diseases, autoimmune gastritis, ulcerative colitis,
CC   glomerulonephritis, pulmonary fibrosis, heart failure,
CC   atherosclerosis, aplastic anaemia, myelodisplastic syndromes,
CC   osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
CC   myocardial infarction.
XX
SQ   Sequence 1066 BP; 178 A; 367 C; 335 G; 186 T; 0 other;
```

```
  Query Match             100.0%;  Score 813;  DB 21;  Length 1066;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 199

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 259

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 319

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db    320 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 379

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    380 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 439

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    440 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 499

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    500 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 559

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    560 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 619

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    620 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 679
```

```
Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     680 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 739

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     740 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 799

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     800 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 859

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     860 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 919

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
           |||||||||||||||||||||||||||||||||
Db     920 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 952
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RESULT 13
AAV39085
ID AAV39085 standard; cDNA; 1077 BP.
XX
AC AAV39085;
XX
DT 26-OCT-1998 (first entry)
XX
DE Human tumour necrosis factor receptor-6 alpha cDNA.
XX
KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW endothelial cells; keratinocytes; normal prostate; apoptosis;
KW prostate tumour tissue; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	25..927
FT		/*tag= a
FT		/product= "TNFR-6 alpha protein"
FT	sig_peptide	25..114
FT		/*tag= b
FT	mat_peptide	115..924
FT		/*tag= c

XX
PN WO9830694-A2.
XX
PD 16-JUL-1998.
XX
PF 13-JAN-1998; 98WO-US00153.
XX
PR 14-JAN-1997; 97US-0035496.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
XX
DR WPI; 1998-399142/34.
DR P-PSDB; AAW63622.
XX
PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
PT the diagnosis of immune system-related disorder(s)
XX
PS Disclosure; Fig 1; 91pp; English.
XX
CC The present sequence represents the human tumour necrosis factor
CC receptor-6 alpha (TNFR-6 alpha) cDNA. The invention also provides
CC for the TNFR-6 beta cDNA (AAV39086). TNFR-6 alpha and TNFR-6 beta are
CC members of the tumour necrosis factor receptor (TNFR) family. TNFRs
CC are expressed in endothelial cells, keratinocytes, normal prostate and
CC prostate tumour tissue. For a number of disorders of these cells,
CC particularly of the immune system, substantially altered (whether
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
CC polypeptides, nucleic acids and antibodies are claimed to be useful in
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
CC also claimed to be useful for identifying ligands which may be useful
CC in the treatment of apoptosis related disorders.
XX
SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

Query Match 100.0%; Score 813; DB 19; Length 1077;
Best Local Similarity 100.0%; Pred. No. 5.1e-145;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db     112 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 171

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 231

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 291

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 351

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db     352 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 411

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 471

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 531

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 591

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 651

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     652 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 711

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 771

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     772 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 831

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 891

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
           |||||||||||||||||||||||||||||||||
Db     892 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 924
```

RESULT 14

```
AAA37772
ID   AAA37772 standard; DNA; 1077 BP.
XX
AC   AAA37772;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Human tumour necrosis factor receptor-6 alpha coding sequence.
XX
KW   Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;
KW   ocular neovascularisation; solid tumour; malignancy; prostate cancer;
KW   breast cancer; colon cancer; diabetic retinopathy; microbial infection;
KW   pre-maturity macular degeneration; allergy; inflammation; tissue damage;
KW   thyroid associated opthalmopathy; cell damage; parasitic infection;
KW   bone disease; osteoporosis; atherosclerosis; cardiovascular disease;
KW   neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW   graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
KW   psoriasis; septic shock; ulcerative colitis; therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             25..927
FT                   /*tag=  a
FT                   /product= TNFR-6alpha
XX
PN   WO200052028-A1.
XX
PD   08-SEP-2000.
XX
PF   03-MAR-2000; 2000WO-US05686.
XX
PR   04-MAR-1999;   99US-0121774.
PR   12-MAR-1999;   99US-0124092.
PR   27-APR-1999;   99US-0131279.
PR   30-APR-1999;   99US-0131964.
PR   02-AUG-1999;   99US-0146371.
PR   01-DEC-1999;   99US-0168235.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Gentz RL,  Ni J,  Ebner R,  Yu G,  Ruben SM,  Feng P;
XX
DR   WPI; 2000-572174/53.
DR   P-PSDB; AAY90357.
XX
PT   Nucleic acids encoding human tumour necrosis factor receptor (TNFR)
PT   proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.
PT   Alzheimer's disease, osteoporosis and graft rejection -
XX
PS   Claim 2; Fig 1; 332pp; English.
XX
CC   This sequence encodes the human tumour necrosis factor receptor 6
CC   alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA
CC   and protein sequences can be used in the prevention, treatment and
CC   diagnosis of diseases associated with inappropriate TNFR expression. The
CC   nucleic acids, polypeptides, antibodies, agonists and antagonists against
CC   them may be used for the treatment of a range of conditions such as
CC   disorders associated with neovascularisation (especially ocular
CC   neovascularisation) (such as solid tumours and malignancies (e.g.
CC   prostate cancer, breast cancer and colon cancer), diabetic retinopathy
CC   and pre-maturity macular degeneration), allergies, inflammation,
CC   thyroid associated opthalmopathy tissue/cell damage, wounds, microbial
CC   and parasitic infections, bone disease (e.g. osteoporosis),
CC   atherosclerosis, pain, cardiovascular disease (e.g. stroke),
CC   neurodegenerative disorders (e.g. Alzheimer's disease), immune
CC   disorders (e.g. graft rejection), rheumatism, liver disease,
CC   autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative
CC   colitis.
XX
SQ   Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

  Query Match             100.0%;  Score 813;  DB 21;  Length 1077;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db     112 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 171

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 231

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 291

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 351

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 411

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 471

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Db     472 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 531

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 591

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
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Db     592 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 651

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     652 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 711

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 771

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     772 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 831

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 891

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||
Db     892 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 924


RESULT 15
AAD33281
ID   AAD33281 standard; cDNA; 1077 BP.
XX
AC   AAD33281;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human tumour necrosis factor receptor (TNFR)-6alpha cDNA.
XX
KW   Human; tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;
KW   immune system-related disorder; inflammatory disease; immunosuppressive;
KW   bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;
```

```
KW   autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW   multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;
KW   graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;
KW   neuroprotective; antiarteriosclerotic; dermatological; asthma; receptor;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "Human TNFR-6alpha protein"
FT   sig_peptide     1..114
FT                   /*tag=  b
FT   mat_peptide     115..924
FT                   /*tag=  c
FT                   /product= "Human mature TNFR-6alpha protein"
XX
PN   WO200218622-A2.
XX
PD   07-MAR-2002.
XX
PF   24-AUG-2001; 2001WO-US26396.
XX
PR   25-AUG-2000; 2000US-227598P.
PR   21-NOV-2000; 2000US-252131P.
PR   06-JUL-2001; 2001US-303224P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Gentz RL,  Ebner R,  Yu G,  Ruben SM,  Ni J,  Feng P;
XX
DR   WPI; 2002-281068/32.
DR   P-PSDB; AAE20848.
XX
PT   Novel nucleic acid molecules comprising a polynucleotide encoding human
PT   tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides
PT   useful for treating disease e.g. inflammatory and autoimmune disorders
PT   -
XX
PS   Example 1; Fig 1; 350pp; English.
XX
CC   The invention relates to human tumour necrosis factor receptor (TNFR)-
CC   6alpha and 6beta protein and their corresponding nucleic acids. The
CC   invention provides screening methods for identifying agonists and
CC   antagonists of TNFR-6alpha and 6beta activity. The invention also
CC   provides diagnostic and therapeutic methods for detecting and treating
CC   immune system-related disorders. The method is useful for treating or
CC   preventing an inflammatory disease or disorder selected from bowel
CC   disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
CC   disease or disorder selected from systemic lupus erythematosus,
CC   arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
CC   and autoimmune encephalitis, graft versus host disease (GVHD), and an
CC   allergy or asthma. The present sequence is human TNFR-6alpha cDNA.
XX
SQ   Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;
```

```
  Query Match             100.0%;  Score 813;  DB 24;  Length 1077;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-145;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
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Db     112 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 171

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db     172 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 231

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 291

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db     292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 351

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 411

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 471

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 531

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 591

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 651

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     652 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 711

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 771

Qy     661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     772 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 831

Qy     721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 891

Qy     781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db     892 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 924
```

```
Search completed: January  6, 2003, 13:55:32
Job time : 233 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 13:45:41 ; Search time 1966 Seconds
(without alignments)
6697.320 Million cell updates/sec

Title: US-09-936-024-2
Perfect score: 813
Sequence: 1 gtggcagaaacacccaccta.....agcgcttcctccctgtgcac 813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	657	80.8	1118	13	BI821789	BI821789 603035863
	2	594	73.1	617	12	BE878908	BE878908 601492609
c	3	577.4	71.0	728	14	BM680786	BM680786 UI-E-EO1-
	4	577	71.0	679	12	BE878006	BE878006 601489784
	5	573.8	70.6	863	14	BQ687526	BQ687526 AGENCOURT
	6	567.2	69.8	572	14	BM767535	BM767535 K-EST0050
	7	541.8	66.6	1203	13	BM480312	BM480312 AGENCOURT
	8	529	65.1	1037	12	BG679499	BG679499 602627514
	9	499.8	61.5	874	12	BF339551	BF339551 602039016
c	10	482.6	59.4	692	10	AW083241	AW083241 xc07a04.x
c	11	466.8	57.4	600	10	AW262121	AW262121 xq31d04.x
c	12	458	56.3	568	14	BQ019285	BQ019285 UI-H-DT1-
	13	428.6	52.7	588	13	BI838357	BI838357 603083306
	14	421.6	51.9	551	12	BE879166	BE879166 601486906
c	15	411.6	50.6	540	10	AW471440	AW471440 xw59e06.x
	16	405	49.8	606	14	BM767446	BM767446 K-EST0049
	17	400.2	49.2	605	14	BM767088	BM767088 K-EST0049
	18	400.2	49.2	605	14	BM767418	BM767418 K-EST0049
	19	393.8	48.4	616	14	BM743072	BM743072 K-EST0016
	20	392.8	48.3	596	14	BM767064	BM767064 K-EST0049
	21	389.4	47.9	554	10	AW464298	AW464298 BP230015A
	22	388.4	47.8	1216	14	BQ716334	BQ716334 AGENCOURT
c	23	387.2	47.6	514	10	AW662363	AW662363 hi25f01.x
	24	387	47.6	588	14	BM756087	BM756087 K-EST0034
	25	387	47.6	593	14	BM759026	BM759026 K-EST0038
	26	383.8	47.2	486	14	BM831338	BM831338 K-EST0105
c	27	381.4	46.9	475	9	AI718743	AI718743 as95h04.x
	28	377	46.4	697	12	BE873766	BE873766 601483915
c	29	359	44.2	478	12	BF001490	BF001490 7g88h10.x
c	30	354	43.5	515	10	AW083914	AW083914 xc25g02.x
c	31	345.2	42.5	459	10	AW014771	AW014771 UI-H-BI0-
	32	339.8	41.8	384	14	BM738195	BM738195 K-EST0002
c	33	336.4	41.4	448	14	BM672727	BM672727 UI-E-CQ0-
c	34	324	39.9	445	9	AI857725	AI857725 wl21a08.x
	35	315.2	38.8	524	14	BM833454	BM833454 K-EST0108
c	36	311.8	38.4	453	10	AW204999	AW204999 UI-H-BI1-
c	37	308.8	38.0	467	9	AA025673	AA025673 ze90h09.s
c	38	308	37.9	436	9	AI290210	AI290210 ql79g12.x
c	39	305	37.5	452	10	AW771720	AW771720 hl71a02.x
c	40	300	36.9	430	9	AI561219	AI561219 tq27c11.x
	41	292.8	36.0	500	14	BM833463	BM833463 K-EST0108
c	42	286	35.2	468	10	AW769220	AW769220 hl54h07.x
c	43	282.4	34.7	340	10	AW316995	AW316995 xx10e06.x
c	44	281.8	34.7	417	10	AW006931	AW006931 wt08b06.x
c	45	280	34.4	405	9	AI520716	AI520716 ti06f10.x

ALIGNMENTS

RESULT 1
BI821789
LOCUS BI821789 1118 bp mRNA linear EST 04-OCT-2001
DEFINITION 603035863F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176910 5', mRNA sequence.
ACCESSION BI821789
VERSION BI821789.1 GI:15933339
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1118)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11440 row: n column: 15
High quality sequence stop: 758.
FEATURES Location/Qualifiers
source 1. .1118

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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5176910"
                     /clone_lib="NIH_MGC_115"
                     /lab_host="DH10B"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
BASE COUNT      223 a    377 c    339 g    179 t
ORIGIN

  Query Match             80.8%;  Score 657;  DB 13;  Length 1118;
  Best Local Similarity   99.4%;  Pred. No. 2.2e-113;
  Matches  701;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    4;

Qy    110 GCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGG 169
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCCCCACGACGTGTGG-CCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGG 59

Qy    170 A-GCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGC 228
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 AGGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGC 119

Qy    229 CACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTC 288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 CACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTC 179

Qy    289 TGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGC 348
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    180 TGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGA-TGCCCCGGGCACCCCCAGC 238

Qy    349 CAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCA 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 CAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCA 298

Qy    409 GAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGC 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 GAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGC 358

Qy    469 TCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTA 528
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    359 TCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCA-GGTA 417

Qy    529 CCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCC 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 CCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCC 477

Qy    589 ATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACA 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 ATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACA 537

Qy    649 CCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTG 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 CCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTG 597

Qy    709 GGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATG 768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 GGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATG 657

Qy    769 CCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||||||||||||||
Db    658 CCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 702


RESULT 2
BE878908
```

```
LOCUS       BE878908                617 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601492609F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894794 5',
            mRNA sequence.
ACCESSION   BE878908
VERSION     BE878908.1  GI:10327684
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9685  row: a  column: 03
            High quality sequence stop: 617.
FEATURES             Location/Qualifiers
     source          1. .617
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3894794"
                     /clone_lib="NIH_MGC_69"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
BASE COUNT       91 a    224 c    203 g     99 t
ORIGIN

  Query Match             73.1%;  Score 594;  DB 12;  Length 617;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-101;
  Matches  605;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy    156 CTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGA 215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 CTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGA 62

Qy    216 GGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 GGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGC 122

Qy    276 GCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 GCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCC 182

Qy    336 GGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAG 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 GGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAG 242

Qy    396 CAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 CAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCT 302

Qy    456 CAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCT 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 CAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCT 362

Qy    516 CAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTT 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 CAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTT 422

Qy    576 CCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGG 635
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Db    423 CCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGG 482

Qy    636 CTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCT 695
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Db    483 CTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCT 542

Qy    696 CACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCG 755
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    543 CACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGG-TGCTGCAGGCGCTGCG 601

Qy    756 CGTGGC 761
          ||||||
Db    602 CGTGGC 607


RESULT 3
BM680786/c
LOCUS       BM680786                728 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  UI-E-EO1-ajc-j-12-0-UI.s1 UI-E-EO1 Homo sapiens cDNA clone
            UI-E-EO1-ajc-j-12-0-UI 3', mRNA sequence.
ACCESSION   BM680786
VERSION     BM680786.1  GI:18990682
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .728
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EO1-ajc-j-12-0-UI"
                     /clone_lib="UI-E-EO1"
                     /tissue_type="fetal eye"
                     /dev_stage="fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EO1 is a normalized cDNA library containing the
                     following tissue(s): fetal eye. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CGCGTATACC. This library was created for the program, Gene
                     Discovery in the Visual System, supported by National Eye
                     Institute (NEI).
                     TAG_LIB=UI-E-EO1
                     TAG_TISSUE=human fetal eye
                     TAG_SEQ=CGCGTATACC"
BASE COUNT      133 a    218 c    248 g    129 t
ORIGIN

  Query Match             71.0%;  Score 577.4;  DB 14;  Length 728;
  Best Local Similarity   99.3%;  Pred. No. 1.7e-98;
  Matches  591;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy    222 GGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGC 281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 GGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGC 646

Qy    282 TGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCAC 341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 TGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCAC 586

Qy    342 CCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTC 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 CCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTC 526

Qy    402 CAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGT 461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 CAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGT 466

Qy    462 GCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCAC 521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 GCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCAC 406

Qy    522 CAGGGTAC---CAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCA 578
          ||||||||   ||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    405 CAGGGTACCAGCAGGAGCTGAGGAGTGTGAGCGTCCCGTCATCGACTTTGTGGCTTTCCA 346

Qy    579 GGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTG 638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 GGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTG 286

Qy    639 GGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCAC 698
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Db    285 GGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCAC 226

Qy    699 GGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGT 758
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 GGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGT 166

Qy    759 GGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 GGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 111


RESULT 4
BE878006
LOCUS       BE878006                679 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601489784F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891908 5',
            mRNA sequence.
ACCESSION   BE878006
VERSION     BE878006.1  GI:10326782
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM9677  row: h  column: 21
           High quality sequence stop: 672.
FEATURES             Location/Qualifiers
     source          1. .679
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3891908"
                     /clone_lib="NIH_MGC_69"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      113 a    239 c    204 g    123 t
ORIGIN

  Query Match             71.0%;  Score 577;  DB 12;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-98;
  Matches  577;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    237 CCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGA 296
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Db     11 CCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGA 70

Qy    297 GCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACAC 356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 GCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACAC 130

Qy    357 GCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTG 416
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Db    131 GCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTG 190

Qy    417 CCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTC 476
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Db    191 CCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTC 250

Qy    477 CCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGC 536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 CCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGC 310

Qy    537 TGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAG 596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 TGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAG 370

Qy    597 GCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGC 656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 GCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGC 430

Qy    657 GGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCA 716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 GGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCA 490

Qy    717 GGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCT 776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 GGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCT 550

Qy    777 GGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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Db    551 GGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 587


RESULT 5
BQ687526
LOCUS       BQ687526                 863 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8345883 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250691
            5', mRNA sequence.
ACCESSION   BQ687526
VERSION     BQ687526.1  GI:21812842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2394  row: c  column: 12
           High quality sequence stop: 599.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_110"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of  California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      133 a    312 c    276 g    141 t      1 others
ORIGIN

  Query Match             70.6%;  Score 573.8;  DB 14;  Length 863;
  Best Local Similarity   94.8%;  Pred. No. 8e-98;
  Matches  637;  Conservative    0;  Mismatches   28;  Indels    7;  Gaps    4;

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Db    149 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGT 208

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    209 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 268

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    269 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 328

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    329 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 388

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db    389 AACCGCGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 448

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db    449 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 508

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Db    509 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGTTCCAGCTCAGAGCAGTGCCAG 568

Qy    421 CCCCACCGCAACTGCACGG--CCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCC 478
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Db     569 CCCCACCGCAACTGCACGNGCCCTGGGCCTGGGCCCTCAATGTGCCAGGCTCTTCCTCCC 628

Qy     479 ATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGA--GC 536
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Db     629 ATGACACGCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAAGCT 688

Qy     537 TGAGGAGTGTGAGCGTGCCGTCATCGAC-TTTGTGGCTTTCCAGGACATCTCCATCAAGA 595
           | |||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     689 GAGGAAGTGTGAGCGTGCCGTCATCGACTTTTGTGGCTTTCCAGGACATCTCCATCAAGA 748

Qy     596 GGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGA--GGGCTGGGGTCCGACACCAAG 653
           ||||||||||||||||||||||||||||||||||||  ||   ||||||||| ||| |
Db     749 AGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAAGGGCTGGGGGTCCGAAACCCAA 808

Qy     654 GGCGGGCCGCGC 665
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Db     809 GGGCGGGGCCGC 820
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RESULT 6
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LOCUS       BM767535                572 bp    mRNA    linear   EST 04-MAR-2002
DEFINITION  K-EST0050015 S1SNU5s2 Homo sapiens cDNA clone S1SNU5s2-3-E03 5',
            mRNA sequence.
ACCESSION   BM767535
VERSION     BM767535.1  GI:19097150
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 3  row: E  column: 03
            High quality sequence stop: 572.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="S1SNU5s2"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Lymphoblast-like"
                     /cell_line="SNU-5"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library. After analyzing and
                     sequencing about 2,000 ~ 3,000 colonies in original cDNA
                     library, the abundant cDNAs were selected and amplified by
                     PCR reaction using vector region primer including T7
                     promotor as 5' primer and N(dT)14 as 3' primer. The PCR
                     products were used as template for synthesis of
                     biotinylated single stranded RNA by in vitro transcription
                     reaction. The synthesized RNA probes were hybridized with
                     antisense single stranded cDNAs prepared from original
                     liberary and incubated with avidin-gel. After removing
                     DNA-RNA hybrids by centrifuge, the subtracted cDNA
                     libraries were constructed by transformaion of the
                     remaining DNA into competent cells E. coli Top10F' with
                     electroporation method."
BASE COUNT      90 a    213 c    174 g     95 t
ORIGIN
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  Query Match             69.8%;  Score 567.2;  DB 14;  Length 572;
  Best Local Similarity   99.5%;  Pred. No. 1.3e-96;
  Matches  569;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     117 GACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTG 176
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Db       1 GACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTG 60

Qy     177 CCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCAC 236
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Db      61 CCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCAC 120

Qy     237 CCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGA 296
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Db     121 CCACAACCGCGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGA 180

Qy     297 GCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACAC 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACAC 240

Qy     357 GCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTG 416
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     241 GCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGTTCCAGCTCAGAGCAGTG 300

Qy     417 CCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTC 476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTC 360

Qy     477 CCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGC 536
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Db     361 CCATGACACGCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGC 420

Qy     537 TGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAG 596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAG 480

Qy     597 GCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGC 656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGC 540

Qy     657 GGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTC 688
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Db     541 GGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTC 572
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RESULT 7
BM480312
LOCUS       BM480312                1203 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6424187 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491790
            5', mRNA sequence.
ACCESSION   BM480312
VERSION     BM480312.1  GI:18529354
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 1203)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12112  row: n  column: 15
            High quality sequence start: 4
            High quality sequence stop: 560.
FEATURES             Location/Qualifiers
     source          1. .1203
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5491790"
                     /clone_lib="NIH_MGC_67"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      202 a    452 c    311 g    238 t
ORIGIN

  Query Match             66.6%;  Score 541.8;  DB 13;  Length 1203;
  Best Local Similarity   96.9%;  Pred. No. 8.3e-92;
  Matches  596;  Conservative    0;  Mismatches   12;  Indels    7;  Gaps    4;

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Db    193 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 252

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 312

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 372

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 432

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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Db    433 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 492

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db    493 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 552

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 612

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
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Db    613 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 672

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAG-CTGA 539
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Db    673 GACACCCTGTGCACCCGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAAGAGCCTGA 732

Qy    540 GGAGTGTGAGCGTG--CCGTCATCGACTTTGTGG--CTTTCCAGGACATCTCCAT--CAA 593
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Db    733 GGAGTGTGAGCGTGCCCCCTCCATCCACTTTGTGGGCTTTTCCAGGACCTCTTCCTTCAAA 792

Qy    594 GAGGCTGCAGCGGCT 608
          ||| ||||||||||
Db    793 AAGGTTGCAGCGGCT 807


RESULT 8
BG679499
LOCUS       BG679499               1037 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602627514F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752507 5',
            mRNA sequence.
ACCESSION   BG679499
VERSION     BG679499.1  GI:13910896
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1037)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10610  row: k  column: 04
            High quality sequence stop: 762.
FEATURES             Location/Qualifiers
     source          1. .1037
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4752507"
                     /clone_lib="NCI_CGAP_Skn4"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library  constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      153 a    364 c    337 g    183 t
ORIGIN

  Query Match             65.1%;  Score 529;  DB 12;  Length 1037;
  Best Local Similarity   85.9%;  Pred. No. 2e-89;
  Matches  707;  Conservative    0;  Mismatches   95;  Indels   21;  Gaps   10;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    195 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 254

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 314

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    315 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTAGAGCGCTGCCGC 374

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 434

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    435 AACCGTGCCTGCCGCTG-CGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 493
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```
Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     494 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 553

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     554 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 613

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
           |||||||||||||| ||||||||||||||||||||||||||||||||||||| ||||
Db     614 CCCCACCGCAACTGC-CGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTTCCAT 672

Qy     481 GACACCCTG-TGCACCAGCTGCAC-TGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTG 538
           |||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Db     673 GACACCCTGTTGCACCAGCTGCACTTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTG 732

Qy     539 AGGAGTGTG-AGCGTGCCGT-CATCGACTTTGTGGCTTTCC--------AGGACATCTCC 588
           ||||||||| |||||||||| |||||||||||||  || |          | | |
Db     733 AGGAGTGTGAAGCGTGCCGTCCATCGACTTTGTGGGCTTTCCCAGGGAACATCTTCCATC 792

Qy     589 ATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCT---CGAGGCCCCGGAGGGCTGGGGTCCG 645
           |  |||         | || ||  |||||||||      |||||||  ||   ||| ||||
Db     793 AAGAAGGCTTGCAGGGGGTTGTGGCAGGCCCTTCCGAAGGCCCCGAGGGCTGGGGTTCCG 852

Qy     646 ACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTC 705
           ||||||||||||||   | | |          |   |||||||||| ||   | | |
Db     853 ACACCAAGGGCGGGCGCCCGGCCTGCAGCTTGAAGCTTGCGTCGGCGGGTCCACGGGAGC 912

Qy     706 CTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGG 765
             |||| || | | |  | |  |||| ||  ||  |||  ||||||| |||||||| |
Db     913 TCCGGGGGGCCGCAAGAAGGGGCGCTGCTGGTGCGCCTGTCGGCGCTG-GCGTGGCCTG- 970

Qy     766 ATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTG 808
             | |||||||||||||| | | | |  | |||   |||
Db     971 --ATGCCGGCTGGAGCGGAGCGCCGGAGCGTTCCTCCCGGCTG 1011


RESULT 9
BF339551
LOCUS       BF339551                874 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  602039016F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186995
            5', mRNA sequence.
ACCESSION   BF339551
VERSION     BF339551.1  GI:11286006
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9508  row: p  column: 04
            High quality sequence stop: 701.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4186995"
                     /clone_lib="NCI_CGAP_Brn64"
                     /tissue_type="glioblastoma with EGFR amplification"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      129 a    299 c    301 g    145 t
ORIGIN

  Query Match           61.5%;  Score 499.8;  DB 12;  Length 874;
  Best Local Similarity  87.8%;  Pred. No. 5.7e-84;
  Matches  568;  Conservative    0;  Mismatches   77;  Indels    2;  Gaps    2;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 244

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 304

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     305 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 364

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     365 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 424

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 484

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     485 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 544

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
           |||||||    |||||  | ||||||||||||||||||||||||||||||||||||||
Db     545 TGCCAGCGTGCCCCCCAGGCAACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 604

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
           ||||||||  |||||||||||||  ||||||||||||||||||||||||||||||||||||
Db     605 CCCCACCG-AACTGCACGGCCTGGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 663

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
           ||||||||||   |          | |||||||||||| ||||||||  |        |
Db     664 GACACCCTGTGGCACCAGCTGCACTGGTTCCCCCTCAGCA-CAGGGTACAGGAGTTGATG 722

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
           |||||||||||||||| ||    ||   |  |||||||   ||||||||||||||
Db     723 AAGTGTGAGCGTGCCGTCTTCTGAGTTTGTGGCTTCCAGGGACTCTCCATCAAGAGGTGC 782

Qy     601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGAC 647
             |  |  |      | ||  ||||    |   | | ||||  || |
Db     783 GCGGTGTGGGCCTTAGGCCCGGAGGTGGGGTCCGCCAGGGGGGCGGC 829


RESULT 10
AW083241/c
LOCUS       AW083241                692 bp    mRNA    linear   EST 14-OCT-1999
DEFINITION  xc07a04.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583534 3'
            similar to TR:O95407 O95407 DECOY RECEPTOR 3. ;contains L1.b1 MER22
            repetitive element ;, mRNA sequence.
ACCESSION   AW083241
VERSION     AW083241.1  GI:6038393
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
```

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 414.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2583534"
                     /clone_lib="NCI_CGAP_Co21"
                     /tissue_type="moderately differentiated adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Normalized to Cot >500.   Average insert size 1.04kb.
                     Normalized version of NCI_CGAP_Co18.   Library constructed
                     by Life Technologies."
BASE COUNT      136 a    205 c    235 g    115 t      1 others
ORIGIN

  Query Match             59.4%;  Score 482.6;  DB 10;  Length 692;
  Best Local Similarity   97.7%;  Pred. No. 9.1e-81;
  Matches  510;  Conservative    0;  Mismatches   10;  Indels    2;  Gaps    2;

Qy     293 TGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGA 352
           |||||||||||||||||||||| |||||||||||||||||||||||||    |||||
Db     619 TGGAGCACGCATCGTGTCCACCT-GTGCCGGCGTGATTGCCCCGGGCACCCCAGTCCAGA 561

Qy     353 ACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGC 412
           |||||||||||||||||||||| ||||||||||||||    ||||||||||||||||
Db     560 ACACGCAGTGCCAGCCGTGCCCCCNAGGCACCTTCTCAGCAGCAAGCTCCAGCTCAGAGC 501

Qy     413 AGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTT 472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     500 AGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTT 441

Qy     473 CCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAG 532
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     440 CTTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAG 381

Qy     533 GAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCA 592
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     380 GAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCA 321

Qy     593 AGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAA 652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     320 AGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAA 261

Qy     653 GGGCGGGCCGCGCGGCCTTGCAGCTGAAGC-TGCGTCGGCGGCTCACGGAGCTCCTGGGG 711
           |||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Db     260 GGGCGGGCCGCGCGGCCTTGCAGCTGAAACTTGCGTCGGCGGCTCACGGAGCTCCTGGGG 201

Qy     712 GCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCC 771
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200 GCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCC 141

Qy     772 GGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
           |||||||||||||||||||||||||||||||||||||||||||
Db     140 GGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 99


RESULT 11
AW262121/c
LOCUS       AW262121                 600 bp    mRNA    linear   EST 28-DEC-1999
DEFINITION  xq31d04.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752231 3'
            similar to TR:O95407 O95407 DECOY RECEPTOR 3. ;contains TAR1.b1
            TAR1 repetitive element ;, mRNA sequence.
ACCESSION   AW262121
VERSION     AW262121.1  GI:6638937
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Possible reversed clone: polyT not found
            Seq primer: -40UP from Gibco
            High quality sequence stop: 410.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2752231"
                     /clone_lib="NCI_CGAP_Lu28"
                     /tissue_type="two pooled squamous cell carcinomas"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies."
BASE COUNT      120 a    177 c    199 g    102 t      2 others
ORIGIN

  Query Match             57.4%;  Score 466.8;  DB 10;  Length 600;
  Best Local Similarity   98.1%;  Pred. No. 8.1e-78;
  Matches  471;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy     334 CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCC 393
           || ||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 CCCGGGCACCCAGCCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCC 541

Qy     394 AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC 453
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||
Db     540 AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCNTGGGCNTGGCC 481

Qy     454 CTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 CTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC 421

Qy     514 CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT 361

Qy     574 TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAG 301

Qy     634 GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGG 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGG 241

Qy     694 CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTG 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTG 181
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Qy    754 CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 121


RESULT 12
BQ019285/c
LOCUS       BQ019285                568 bp    mRNA    linear   EST 17-JUN-2002
DEFINITION  UI-H-DT1-awn-l-19-0-UI.s1 NCI_CGAP_DT1 Homo sapiens cDNA clone
            IMAGE:5891874 3', mRNA sequence.
ACCESSION   BQ019285
VERSION     BQ019285.1  GI:19754562
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 568)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5891874"
                     /clone_lib="NCI_CGAP_DT1"
                     /tissue_type="Metastatic Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_DT1 is a normalized cDNA library containing the
                     following tissue(s): Metatastic Chondrosarcoma in Lung.
                     The library was constructed according to Bonaldo, Lennon
                     and Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site. Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
                     used to prime the synthesis of first-strand cDNA contains
                     a library tag sequence that is located between the Not I
                     site and the (dT)18 tail. The sequence tag for this
                     library is AACTGTTCGG.
                     TAG_LIB=UI-H-DT1
                     TAG_TISSUE=lung metatastic chondrosarcoma
                     TAG_SEQ=AACTGTTCGG"
BASE COUNT      106 a    170 c    187 g    105 t
ORIGIN

  Query Match             56.3%;  Score 458;  DB 14;  Length 568;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-76;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    356 CGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGT 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 CGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGT 509

Qy    416 GCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCT 475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 GCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCT 449

Qy    476 CCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAG 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 CCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAG 389

Qy    536 CTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGA 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 CTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGA 329

Qy    596 GGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGG 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 GGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGG 269

Qy    656 CGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGC 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 CGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGC 209

Qy    716 AGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGC 775
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Db    208 AGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGC 149

Qy    776 TGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
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Db    148 TGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 111


RESULT 13
BI838357
LOCUS       BI838357                588 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603083306F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222545 5',
            mRNA sequence.
ACCESSION   BI838357
VERSION     BI838357.1  GI:15949907
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11559  row: 1  column: 02
            High quality sequence stop: 588.
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     source          1. .588
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5222545"
                     /clone_lib="NIH_MGC_120"
                     /lab_host="DH10B"
                     /note="Organ: pooled pancreas and spleen; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of spleen and pancreas from 28 yo
                     male.  Library is oligo-dT primed and directionally cloned
                     (EcoRV  site is destroyed upon cloning).  Average insert
                     size 1.5 kb, insert size range 1-2.5 kb.  Library is
                     normalized and enriched for  full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT       97 a    224 c    171 g     95 t      1 others
ORIGIN

  Query Match             52.7%;  Score 428.6;  DB 13;  Length 588;
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Qy    100 CGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGG 159
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Db      1 CGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGG 60

Qy    160 AACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCA 219
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Db     61 AACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCA 120

Qy    220 CGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCAC 279
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Db    121 CGGGCTTGCCACGCCACCCACAACCGCGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCAC 180

Qy    280 GCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGC 339
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Db    181 GCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGC 240

Qy    340 ACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC 399
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Db    241 ACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGT 300

Qy    400 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT 459
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Db    301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT 360

Qy    460 GTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGC 519
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Db    361 GTGCCAGGCTCTTCCTCCCATGACACGCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGC 420

Qy    520 ACCAGGGTACCAGGAG 535
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Db    421 ACCANGGTACCAGGTG 436


RESULT 14
BE879166
LOCUS       BE879166                551 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601486906F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889296 5',
            mRNA sequence.
ACCESSION   BE879166
VERSION     BE879166.1  GI:10327942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9670  row: 1  column: 01
            High quality sequence stop: 546.
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
BASE COUNT       76 a    189 c    190 g     96 t
ORIGIN

  Query Match            51.9%;  Score 421.6;  DB 12;  Length 551;
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  Matches  446;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    2;

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Qy    423 CCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGA 482
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Qy    483 CACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGA 542
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Qy    543 GTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCA 602
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Qy    603 GCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGCCG 662
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Qy    663 CGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGGCGCAGGACGG 722
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Qy    723 GGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAGCG 782
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Db    439 GGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAGCG 498

Qy    783 GAGC-GTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||| ||||||||||||||||||||||||||||
Db    499 GAGCAGTCCGTGAGCGCTTCCTCCCTGTGCAC 530


RESULT 15
AW471440/c
LOCUS       AW471440                540 bp    mRNA    linear   EST 24-FEB-2000
DEFINITION  xw59e06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832322 3'
            similar to TR:O95407 O95407 DECOY RECEPTOR 3. ;contains TAR1.b1
            TAR1 repetitive element ;, mRNA sequence.
ACCESSION   AW471440
VERSION     AW471440.1  GI:7041546
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
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FEATURES             Location/Qualifiers
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
BASE COUNT 120 a 165 c 160 g 88 t 7 others
ORIGIN

Query Match 50.6%; Score 411.6; DB 10; Length 540;
Best Local Similarity 95.2%; Pred. No. 1.7e-67;
Matches 420; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Qy     433 TGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGC 492
           || | |||| ||||| |||||||||||||| |||||||||| |||||||||||| |||||
Db     480 TGTATGGCCNTGGGCNTGGCCCTCAATGTGNCAGGCTCTTCTTCCCATGACACCNTGTGC 421

Qy     493 ACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGT 552
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 ACCAGNTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGT 361

Qy     553 GCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTG 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 GCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTG 301

Qy     613 CAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTG 672
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Qy     673 CAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTG 732
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Qy     733 GTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGT 792
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Qy     793 GAGCGCTTCCTCCCTGTGCAC 813
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Db     120 GAGCGCTTCCTCCCTGTGCAC 100
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Job time : 1973 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 13:48:11 ; Search time 54 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	813	100.0	1164	2	US-08-794-796-1	Sequence 1, Appli
2	813	100.0	1347	4	US-09-286-529-18	Sequence 18, Appl
3	533.4	65.6	1859	4	US-09-286-529-19	Sequence 19, Appl
4	459	56.5	459	4	US-09-286-529-7	Sequence 7, Appli
5	129.6	15.9	525	3	US-08-997-918-47	Sequence 47, Appl
6	112	13.8	2432	3	US-08-974-022-1	Sequence 1, Appli
7	112	13.8	2432	4	US-08-795-445A-1	Sequence 1, Appli
8	112	13.8	2432	4	US-08-795-447A-1	Sequence 1, Appli
9	112	13.8	2432	4	US-08-974-186-1	Sequence 1, Appli
10	112	13.8	2432	4	US-08-795-446B-1	Sequence 1, Appli
11	112	13.8	2432	4	US-08-706-945D-123	Sequence 123, App
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16	110.4	13.6	1324	4	US-08-795-446B-3	Sequence 3, Appli
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18	103	12.7	1355	3	US-08-974-022-5	Sequence 5, Appli
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21	103	12.7	1355	4	US-08-974-186-5	Sequence 5, Appli
22	103	12.7	1355	4	US-08-795-446B-5	Sequence 5, Appli
23	103	12.7	1355	4	US-08-706-945D-127	Sequence 127, App
24	76	9.3	3331	4	US-09-042-785A-1	Sequence 1, Appli
25	68	8.4	759	4	US-09-042-785A-6	Sequence 6, Appli
26	68	8.4	1815	4	US-09-042-785A-24	Sequence 24, Appl
27	68	8.4	2186	3	US-08-959-382-1	Sequence 1, Appli
28	68	8.4	2612	4	US-09-042-785A-3	Sequence 3, Appli
29	68	8.4	2638	4	US-09-042-785A-22	Sequence 22, Appl
30	68	8.4	3474	4	US-09-527-236A-1	Sequence 1, Appli
31	56.4	6.9	1719	4	US-09-042-785A-5	Sequence 5, Appli
c 32	54.8	6.7	1164	2	US-08-794-796-1	Sequence 1, Appli
c 33	54.8	6.7	1347	4	US-09-286-529-18	Sequence 18, Appl
34	52	6.4	2793	1	US-08-209-747-1	Sequence 1, Appli
35	52	6.4	2793	1	US-08-458-298-1	Sequence 1, Appli
36	51.6	6.3	3796	2	US-08-762-308-11	Sequence 11, Appl
37	51.6	6.3	3796	4	US-09-844-634-10	Sequence 10, Appl
38	51.6	6.3	3813	2	US-08-650-000-3	Sequence 3, Appli
39	51.6	6.3	3813	6	5395760-3	Patent No. 5395760
40	49.6	6.1	691	1	US-08-266-080B-12	Sequence 12, Appl
41	49.6	6.1	691	5	PCT-US95-05423-12	Sequence 12, Appl
42	49.6	6.1	705	4	US-09-326-394-3	Sequence 3, Appli
c 43	49.4	6.1	8906	2	US-08-826-267-1	Sequence 1, Appli
44	48.6	6.0	1878	3	US-08-996-139-14	Sequence 14, Appl
45	48.6	6.0	1878	4	US-08-995-659-14	Sequence 14, Appl

ALIGNMENTS

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RESULT 1
US-08-794-796-1
; Sequence 1, Application US/08794796
; Patent No. 5885800
;  GENERAL INFORMATION:
;    APPLICANT:  Emery, John
;    APPLICANT:  Tan, KB
;    APPLICANT:  Truneh, Alem
;    APPLICANT:  Young, Peter
;    TITLE OF INVENTION:  Tumor Necrosis Related Receptor,
;    TITLE OF INVENTION:  TR4
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/794,796
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Han, William T
;      REGISTRATION NUMBER:  34,344
;      REFERENCE/DOCKET NUMBER:  GH50000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5219
;      TELEFAX:  610-270-4026
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1164 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-794-796-1

  Query Match           100.0%;  Score 813;  DB 2;  Length 1164;
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Db    198 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 257

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 497

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db    498 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 557

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
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Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 677

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    678 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 737

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 797

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 857

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 917

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    918 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 977

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||
Db    978 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1010


RESULT 2
US-09-286-529-18
; Sequence 18, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 18
;   LENGTH: 1347
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-286-529-18

  Query Match           100.0%;  Score 813;  DB 4;  Length 1347;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-154;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 464

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 524

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 584

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 644

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 704

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 764

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 824

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 884

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 944

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 1004

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 1064

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 1124

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 1184

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||
Db   1185 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1217


RESULT 3
US-09-286-529-19
; Sequence 19, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
```

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;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 1859
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-286-529-19

  Query Match             65.6%;  Score 533.4;  DB 4;  Length 1859;
  Best Local Similarity   98.9%;  Pred. No. 1.9e-98;
  Matches  537;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 224

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     225 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 284

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     285 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 344

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     345 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 404

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     405 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 464

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     465 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 524

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     525 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 584

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     585 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 644

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     645 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCA 704

Qy     541 GAG 543
          |||
Db     705 GAG 707


RESULT 4
US-09-286-529-7
; Sequence 7, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 459
;   TYPE: DNA
;   ORGANISM: human
US-09-286-529-7

  Query Match             56.5%;  Score 459;  DB 4;  Length 459;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-83;
  Matches  459;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     166 CTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCT 225
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCT 60

Qy     226 TGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGT 285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGT 120

Qy     286 TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC 345
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC 180

Qy     346 AGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGC 405
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGC 240

Qy     406 TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCA 465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCA 300

Qy     466 GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGG 525
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGG 360

Qy     526 GTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATC 585
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATC 420

Qy     586 TCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAG 624
          ||||||||||||||||||||||||||||||||||||||||
Db     421 TCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAG 459


RESULT 5
US-08-997-918-47
; Sequence 47, Application US/08997918
; Patent No. 6077689
; GENERAL INFORMATION:
;  APPLICANT: Snavely, Marshall D.
;  TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS
;  FILE REFERENCE: A-496
;  CURRENT APPLICATION NUMBER: US/08/997,918
;  CURRENT FILING DATE: 1997-12-24
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: fragment encoding amino acids 22-194 of human OPG
US-08-997-918-47

  Query Match             15.9%;  Score 129.6;  DB 3;  Length 525;
  Best Local Similarity   53.6%;  Pred. No. 7.2e-18;
  Matches  270;  Conservative    0;  Mismatches  234;  Indels    0;  Gaps    0;

Qy      11 CACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCC 70
           |||| |  || |        || | ||| ||  |  | | |||| |||||| | | || |
Db      14 CACCTAAATATCTTCATTATGATGAAGAAACTAGTCACCAGCTGCTGTGCGACAAATGTC 73

Qy      71 CCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGT 130
           | || || ||||   || | | ||  |||  |    |  |    ||   || |  || |
Db      74 CTCCGGGTACCTACCTGAAACAGCACTGCACCGCTAAATGGAAAACCGTTTGCGCTCCTT 133

Qy     131 GTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACG 190
           ||||    | | ||||||| | | |||| ||  |   ||   ||||  ||||||
Db     134 GTCCGGACCACTACTACACCGACTCCTGGCACACCTCCGACGAATGCCTGTACTGCTCAC 193
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Qy    191 TCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT 250
          | |||  |||||   || | |    || ||  ||| ||   || ||||||||||  |
Db    194 CGGTTTGCAAGGAGCTGCAGTACGTTAAACAGGAATGCAACCGTACGCACAACCGTGTAT 253

Qy    251 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTC 310
          ||   |||       ||     | | | |     | |||||| || | |||   || ||||
Db    254 GCGAATGCAAAGAAGGTCGTTACCTGGAGATCGAATTCTGCCTGAAACACCGTTCCTGTC 313

Qy    311 CACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGT 370
          | ||||||  ||| ||  |     | || |||||    | |||||    ||| | |  |
Db    314 CGCCTGGTTTCGGTGTTGTACAGGCTGGTACCCCGGAACGTAACACCGTTTGCAAACGTT 373

Qy    371 GCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCA 430
          ||||    ||   ||||||    |   | ||| |||  ||  | |||||     |||  ||
Db    374 GCCCGGACGGTTTCTTCTCCAACGAAACCTCGAGCAAAGCTCCGTGCCGTAAACACACCA 433

Qy    431 ACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGT 490
          |||||| | |   | || ||     | |    |  |||      |  |||| |||| | | |
Db    434 ACTGCTCCGTTTTCGGTCTCCTGTTAACCCAGAAAGGTAACGCTACCCACGACAACATCT 493

Qy    491 GCACCAGCTGCACTGGCTTCCCCC 514
          || || |   | | |  |   |||
Db    494 GCTCCGGTAACTCCGAGTCGACCC 517
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RESULT 6
US-08-974-022-1
; Sequence 1, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, Willaim J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1326
US-08-974-022-1

Query Match 13.8%; Score 112; DB 3; Length 2432;
Best Local Similarity 52.3%; Pred. No. 2.8e-14;

Matches 247; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

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Qy     31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
          ||| |||| || ||    | |||  |||| | | | ||  | || |||||||   |  |
Db    217 GACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAA 276

Qy     91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
          | ||  |||          ||    ||   |||| ||| || ||       |   || ||
Db    277 CAGCACTGCACAGTCAGGAGGAAGACACTGTGTGTCCCTTGCCCTGACTACTCTTATACA 336

Qy    151 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG 210
          |   |||| ||     ||    |||  |||||| |  | | ||| ||| |   ||
Db    337 GACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCCGTGTGCAAGGAACTGCAG 396

Qy    211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
          | |  || ||  ||| ||  ||||||||||||  |  |||   ||       ||   |
Db    397 ACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGC 456

Qy    271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
          | |  | |    |  |||||||| ||||      ||||| || ||    || ||| |
Db    457 TACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTG 516

Qy    331 GCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCA 390
          | || |||||    |  ||||||   ||| |   || ||    ||   |||||||
Db    517 CAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCA 576

Qy    391 GCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTG 450
          |    |  ||      ||  |  ||   |  |||  ||||||||   | || |||||
Db    577 GGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAACTGCAGCTCACTTGGCCTC 636

Qy    451 GCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCA 502
          || | |  |  |||  | |  | |||||||  | ||  || |  ||
Db    637 CTGCTAATTCAGAAAGGAAATGCAACACATGACAATGTATGTTCCGGAAACA 688
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RESULT 7
US-08-795-445A-1
; Sequence 1, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, Willaim J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  124..1326
US-08-795-445A-1

  Query Match             13.8%;  Score 112;  DB 4;  Length 2432;
  Best Local Similarity   52.3%;  Pred. No. 2.8e-14;
  Matches  247;  Conservative    0;  Mismatches  225;  Indels    0;  Gaps    0;

Qy      31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
           ||| |||| || ||    | |||  |||| | | | ||  | || |||||||   |  |
Db     217 GACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAA 276

Qy      91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
           | ||  |||         ||    ||   ||||| ||| || ||       |   || ||
Db     277 CAGCACTGCACAGTCAGGAGGAAGACACTGTGTGTCCCTTGCCCTGACTACTCTTATACA 336

Qy     151 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG 210
           |   |||| ||       ||    |||   ||||||| |  | | ||| |||  |   ||
Db     337 GACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCCGTGTGCAAGGAACTGCAG 396

Qy     211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
           | |  || ||  ||| ||  ||||||||||| |  |||   ||      ||    |
Db     397 ACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGC 456

Qy     271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
           | |  | |    | ||||||||| |||||      ||||| || ||    || ||| |
Db     457 TACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTG 516

Qy     331 GCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCA 390
           | || |||||    | ||||||   ||| |    || ||    ||   |||||||
Db     517 CAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCA 576

Qy     391 GCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTG 450
           |     |  ||      ||  |  ||   |   |||  ||||||||   | || |||||
Db     577 GGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAACTGCAGCTCACTTGGCCTC 636

Qy     451 GCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCA 502
           || | |  |  |||   | |  | |||||||   | ||  || |   ||
Db     637 CTGCTAATTCAGAAAGGAAATGCAACACATGACAATGTATGTTCCGGAAACA 688


RESULT 8
US-08-795-447A-1
; Sequence 1, Application US/08795447A
; Patent No. 6284728
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, William J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  Osteoprotegerin
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  One Amgen Center Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91362-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,447A
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378D2
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  124..1326
US-08-795-447A-1

  Query Match             13.8%;  Score 112;  DB 4;  Length 2432;
  Best Local Similarity   52.3%;  Pred. No. 2.8e-14;
  Matches  247;  Conservative    0;  Mismatches  225;  Indels    0;  Gaps    0;

Qy      31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
           ||| |||| || ||    | |||  |||| | | | ||  | || |||||||   |  |
Db     217 GACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAA 276

Qy      91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
           | ||  |||         ||    ||   ||||| ||| || ||       |   || ||
Db     277 CAGCACTGCACAGTCAGGAGGAAGACACTGTGTGTCCCTTGCCCTGACTACTCTTATACA 336

Qy     151 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG 210
           |   |||| ||       ||    |||   ||||||| |  | | ||| |||  |   ||
Db     337 GACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCCGTGTGCAAGGAACTGCAG 396

Qy     211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
           | |  || ||  ||| ||  ||||||||||| |  |||   ||      ||    |
Db     397 ACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGC 456

Qy     271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
           | |  | |    | ||||||||| |||||      ||||| || ||    || ||| |
Db     457 TACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTG 516

Qy     331 GCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCA 390
           | || |||||    | ||||||   ||| |    || ||    ||   |||||||
Db     517 CAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCA 576

Qy     391 GCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTG 450
           |     |  ||      ||  |  ||   |   |||  ||||||||   | || |||||
Db     577 GGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAACTGCAGCTCACTTGGCCTC 636

Qy     451 GCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCA 502
           || | |  |  |||   | |  | |||||||   | ||  || |   ||
Db     637 CTGCTAATTCAGAAAGGAAATGCAACACATGACAATGTATGTTCCGGAAACA 688


RESULT 9
US-08-974-186-1
; Sequence 1, Application US/08974186
; Patent No. 6284740
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  124..1326
US-08-974-186-1

  Query Match             13.8%;  Score 112;  DB 4;  Length 2432;
  Best Local Similarity   52.3%;  Pred. No. 2.8e-14;
  Matches  247;  Conservative    0;  Mismatches  225;  Indels    0;  Gaps    0;

Qy      31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
           ||| |||| || ||    | |||  |||| | | | ||  | || |||||||    | |
Db     217 GACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAA 276

Qy      91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
           | ||  |||         ||    ||   ||||| ||| || ||      |   || ||
Db     277 CAGCACTGCACAGTCAGGAGGAAGACACTGTGTGTCCCTTGCCCTGACTACTCTTATACA 336

Qy     151 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG 210
            |   |||| ||       ||    |||   ||||||| |  | | ||| |||  |   ||
Db     337 GACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCCGTGTGCAAGGAACTGCAG 396

Qy     211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
           | |  || ||  |||  ||  |||||||||||| |  |||   ||        ||   |
Db     397 ACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGC 456

Qy     271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
           | |  | |    | |||||||| |||||     |||||  || ||    || ||| |
Db     457 TACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTG 516

Qy     331 GCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCA 390
           | || |||||    | ||||||  ||| |   || ||    ||   |||||||
Db     517 CAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCA 576

Qy     391 GCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTG 450
           |     |  ||      ||  |  ||   |  |||  ||||||||   | || |||||
Db     577 GGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAACTGCAGCTCACTTGGCCTC 636

Qy     451 GCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCA 502
             || | |  |  |||   | |  | |||||||   | ||  || |    ||
Db     637 CTGCTAATTCAGAAAGGAAATGCAACACATGACAATGTATGTTCCGGAAACA 688


RESULT 10
US-08-795-446B-1
; Sequence 1, Application US/08795446B
; Patent No. 6288032
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,446B
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  124..1326
US-08-795-446B-1

  Query Match             13.8%;  Score 112;  DB 4;  Length 2432;
  Best Local Similarity   52.3%;  Pred. No. 2.8e-14;
  Matches  247;  Conservative    0;  Mismatches  225;  Indels    0;  Gaps    0;

Qy      31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
           ||| |||| || ||    | |||  |||| | | | ||  | || |||||||    | |
Db     217 GACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAA 276

Qy      91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
           | ||  |||         ||    ||   ||||| ||| || ||      |   || ||
Db     277 CAGCACTGCACAGTCAGGAGGAAGACACTGTGTGTCCCTTGCCCTGACTACTCTTATACA 336

Qy     151 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG 210
            |   |||| ||       ||    |||   ||||||| |  | | ||| |||  |   ||
Db     337 GACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCCGTGTGCAAGGAACTGCAG 396

Qy     211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
           | |  || ||  |||  ||  |||||||||||| |  |||   ||        ||   |
Db     397 ACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGC 456

Qy     271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
           | |  | |    | |||||||| |||||     |||||  || ||    || ||| |
Db     457 TACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTG 516

Qy     331 GCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCA 390
           | || |||||    | ||||||  ||| |   || ||    ||   |||||||
Db     517 CAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCA 576

Qy     391 GCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTG 450
           |     |  ||      ||  |  ||   |  |||  ||||||||   | || |||||
Db     577 GGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAACTGCAGCTCACTTGGCCTC 636

Qy     451 GCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCA 502
             || | |  |  |||   | |  | |||||||   | ||  || |    ||
Db     637 CTGCTAATTCAGAAAGGAAATGCAACACATGACAATGTATGTTCCGGAAACA 688


RESULT 11
US-08-706-945D-123
; Sequence 123, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
```

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;  APPLICANT: Boyle, William
;  APPLICANT:  Lacey, David
;  APPLICANT:  Calzone, Frank
;  APPLICANT:  Chang, Ming-Shi
;  TITLE OF INVENTION: Osteoprotegerin
;  FILE REFERENCE: A-378CIP
;  CURRENT APPLICATION NUMBER: US/08/706,945D
;  CURRENT FILING DATE:  1996-09-03
;  PRIOR APPLICATION NUMBER: 08/577,788
;  PRIOR FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 145
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
;   LENGTH: 2432
;   TYPE: DNA
;   ORGANISM: Rattus rattus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (124)..(1326)
;   OTHER INFORMATION:
US-08-706-945D-123

  Query Match             13.8%;  Score 112;  DB 4;  Length 2432;
  Best Local Similarity   52.3%;  Pred. No. 2.8e-14;
  Matches  247;  Conservative    0;  Mismatches  225;  Indels    0;  Gaps    0;

Qy      31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
           ||| |||| || ||    | |||  |||| | | | ||  | || |||||||   |  |
Db     217 GACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAA 276

Qy      91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
           | ||  |||          ||    ||   ||||| ||| || ||       |   || ||
Db     277 CAGCACTGCACAGTCAGGAGGAAGACACTGTGTGTCCCTTGCCCTGACTACTCTTATACA 336

Qy     151 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG 210
           |   |||| ||       ||    |||   ||||||| |  | | |||  ||| |   ||
Db     337 GACAGCTGGCACACGAGTGATGAATGCGTGTACTGCAGCCCCGTGTGCAAGGAACTGCAG 396

Qy     211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
           | | || ||  |||  ||  ||||||||||| |  |||   ||      ||    |
Db     397 ACCGTGAAACAGGAGTGCAACCGCACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGC 456

Qy     271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
           | |  | |     | |||||||| |||||       |||| || ||    || ||| |
Db     457 TACCTGGAGCTCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTG 516

Qy     331 GCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCA 390
           | || |||||    | ||||||   ||| |    || ||    ||   |||||||
Db     517 CAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCA 576

Qy     391 GCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTG 450
           |     |  ||      ||  |  ||   |   ||| |||||||   | || |||||
Db     577 GGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAACTGCAGCTCACTTGGCCTC 636

Qy     451 GCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCA 502
           || | |  |  |||   | |  | |||||||   | ||  || |   ||
Db     637 CTGCTAATTCAGAAAGGAAATGCAACACATGACAATGTATGTTCCGGAAACA 688


RESULT 12
US-08-974-022-3
; Sequence 3, Application US/08974022
; Patent No. 6015938
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,022
;      FILING DATE:  12-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1324 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1292
US-08-974-022-3

  Query Match             13.6%;  Score 110.4;  DB 3;  Length 1324;
  Best Local Similarity   52.1%;  Pred. No. 5.5e-14;
  Matches  246;  Conservative    0;  Mismatches  226;  Indels    0;  Gaps    0;

Qy      31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
           ||| |||| || ||  | | |||  |||| | | | ||  | || |||||||   |  |
Db     183 GACCCAGAAACTGGTCATCAGCTCCTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAA 242

Qy      91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
           | ||  |||          ||    ||   ||||| ||| || ||     | |   || |||
Db     243 CAGCACTGCACAGTGAGGAGGAAGACATTGTGTGTCCCTTGCCCTGACCACTCTTATACG 302

Qy     151 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG 210
           |   |||| ||  |   ||    ||     || |||| |    | |||  ||| |   ||
Db     303 GACAGCTGGCACACCAGTGATGAGTGTGTGTATTGCAGCCCAGTGTGCAAGGAACTGCAG 362

Qy     211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
           | |   | ||  ||| ||  ||||||||||||| |  ||    ||       ||
Db     363 TCCGTGAAGCAGGAGTGCAACCGCACCCACAACCGAGTGTGTGAGTGTGAGGAAGGGCGT 422

Qy     271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
           | |  | |     |  |||||||| |||||       ||||| || ||  |||||||| |
Db     423 TACCTGGAGATCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCGGGCTCCGGCGTGGTG 482

Qy     331 GCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCA 390
           |  || |||||    | |||||    ||| |    || ||    ||   |||||||
Db     483 CAAGCTGGAACCCCAGAGCGAAACACAGTTTGCAAAAAATGTCCAGATGGGTTCTTCTCA 542

Qy     391 GCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTG 450
           |     |  ||      ||  |  ||       |||   |||||||   |  | |||||
Db     543 GGTGAGACTTCATCGAAAGCACCCTGTATAAAACACACGAACTGCAGCACATTTGGCCTC 602

Qy     451 GCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCA 502
           || | |  |  |||   | |  | |||||||  | ||||  || |   ||
Db     603 CTGCTAATTCAGAAAGGAAATGCAACACATGACAACGTGTGTTCCGGAAACA 654


RESULT 13
US-08-795-445A-3
; Sequence 3, Application US/08795445A
; Patent No. 6284485
;  GENERAL INFORMATION:
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```
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,445A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1324 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1292
US-08-795-445A-3

  Query Match             13.6%;  Score 110.4;  DB 4;  Length 1324;
  Best Local Similarity   52.1%;  Pred. No. 5.5e-14;
  Matches  246;  Conservative    0;  Mismatches  226;  Indels    0;  Gaps    0;

Qy      31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
           ||| |||| || ||  | | |||  |||| | | | ||  | || |||||||    | |
Db     183 GACCCAGAAACTGGTCATCAGCTCCTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAA 242

Qy      91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
           | ||  |||       ||    ||  ||||| ||| || ||    | |   || |||
Db     243 CAGCACTGCACAGTGAGGAGGAAGACATTGTGTGTCCCTTGCCCTGACCACTCTTATACG 302

Qy     151 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG 210
             |  |||| ||  |   ||    ||    || |||| |    | |||  ||| |   ||
Db     303 GACAGCTGGCACACCAGTGATGAGTGTGTGTATTGCAGCCCAGTGTGCAAGGAACTGCAG 362

Qy     211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
           | |   | ||  ||| ||  ||||||||||||  |  ||    ||        ||
Db     363 TCCGTGAAGCAGGAGTGCAACCGCACCCACAACCGAGTGTGTGAGTGTGAGGAAGGGCGT 422

Qy     271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
           | |  | |    |  ||||||||| |||||      |||||  || ||  |||||||| |
Db     423 TACCTGGAGATCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCGGGCTCCGGCGTGGTG 482

Qy     331 GCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCA 390
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RESULT 14
US-08-795-447A-3
; Sequence 3, Application US/08795447A
; Patent No. 6284728
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, William J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  Osteoprotegerin
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  One Amgen Center Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91362-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,447A
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378D2
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1324 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1292
US-08-795-447A-3

  Query Match             13.6%;  Score 110.4;  DB 4;  Length 1324;
  Best Local Similarity   52.1%;  Pred. No. 5.5e-14;
  Matches  246;  Conservative    0;  Mismatches  226;  Indels    0;  Gaps    0;

Qy      31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
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Db     183 GACCCAGAAACTGGTCATCAGCTCCTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAA 242

Qy      91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
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Db     243 CAGCACTGCACAGTGAGGAGGAAGACATTGTGTGTCCCTTGCCCTGACCACTCTTATACG 302

Qy     151 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG 210
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Qy     211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
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Db     363 TCCGTGAAGCAGGAGTGCAACCGCACCCACAACCGAGTGTGTGAGTGTGAGGAAGGGCGT 422

Qy     271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
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RESULT 15
US-08-974-186-3
; Sequence 3, Application US/08974186
; Patent No. 6284740
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1324 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1292
US-08-974-186-3

  Query Match             13.6%;  Score 110.4;  DB 4;  Length 1324;
  Best Local Similarity   52.1%;  Pred. No. 5.5e-14;
  Matches  246;  Conservative    0;  Mismatches  226;  Indels    0;  Gaps    0;

Qy     31 GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
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Db    303 GACAGCTGGCACACCAGTGATGAGTGTGTGTATTGCAGCCCAGTGTGCAAGGAACTGCAG 362

Qy    211 GAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTC 270
             | |   | ||  ||| ||  ||||||||||||| |  ||    ||       ||

Db    363 TCCGTGAAGCAGGAGTGCAACCGCACCCACAACCGAGTGTGTGAGTGTGAGGAAGGGCGT 422

Qy    271 TTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
          | |  | |     |  ||||||||| |||||       |||||  || ||  |||||||| |
Db    423 TACCTGGAGATCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCGGGCTCCGGCGTGGTG 482

Qy    331 GCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCA 390
            | || |||||     |  |||||    ||| |    || ||    ||   ||||||||
Db    483 CAAGCTGGAACCCCAGAGCGAAACACAGTTTGCAAAAAATGTCCAGATGGGTTCTTCTCA 542

Qy    391 GCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTG 450
          |     |  ||      ||  |  ||       |||   |||||||   |  | |||||
Db    543 GGTGAGACTTCATCGAAAGCACCCTGTATAAAACACACGAACTGCAGCACATTTGGCCTC 602

Qy    451 GCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCA 502
            || | |  |  |||   | |  | |||||| | ||||  || |   ||
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OM nucleic - nucleic search, using sw model

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(without alignments)
6062.518 Million cell updates/sec

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Perfect score: 813
Sequence: 1 gtggcagaaacacccaccta.....agcgcttcctccctgtgcac 813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	813	100.0	1114	10	US-09-896-096A-2	Sequence 2, Appli
3	813	100.0	1114	10	US-09-894-924-2	Sequence 2, Appli
4	813	100.0	1347	10	US-09-877-156-18	Sequence 18, Appl
5	809.4	99.6	1137	10	US-09-840-795-1	Sequence 1, Appli
6	533.4	65.6	1859	10	US-09-877-156-19	Sequence 19, Appl
7	515.4	63.4	903	10	US-09-935-727-32	Sequence 32, Appl
8	473.4	58.2	491	10	US-09-896-096A-3	Sequence 3, Appli
9	473.4	58.2	491	10	US-09-894-924-3	Sequence 3, Appli
10	459	56.5	459	10	US-09-877-156-7	Sequence 7, Appli
11	392.2	48.2	1550	10	US-09-935-727-33	Sequence 33, Appl
12	387.4	47.7	1667	10	US-09-935-727-3	Sequence 3, Appli
13	387	47.6	1796	10	US-09-935-727-28	Sequence 28, Appl
14	245.2	30.2	271	10	US-09-896-096A-5	Sequence 5, Appli
15	245.2	30.2	271	10	US-09-894-924-5	Sequence 5, Appli
16	242.2	29.8	283	10	US-09-896-096A-10	Sequence 10, Appl
17	242.2	29.8	283	10	US-09-894-924-10	Sequence 10, Appl
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21	200	24.6	201	10	US-09-896-096A-6	Sequence 6, Appli
22	200	24.6	201	10	US-09-894-924-6	Sequence 6, Appli
23	194.2	23.9	199	10	US-09-896-096A-8	Sequence 8, Appli
24	194.2	23.9	199	10	US-09-894-924-8	Sequence 8, Appli
25	183	22.5	233	9	US-09-292-758-141	Sequence 141, App
26	179	22.0	191	10	US-09-935-727-18	Sequence 18, Appl
27	152.2	18.7	277	10	US-09-896-096A-7	Sequence 7, Appli
28	152.2	18.7	277	10	US-09-894-924-7	Sequence 7, Appli
29	103.4	12.7	564	10	US-09-062-113-102	Sequence 102, App
30	103	12.7	594	10	US-09-062-113-97	Sequence 97, Appl
31	103	12.7	819	10	US-09-062-113-96	Sequence 96, Appl
32	103	12.7	966	10	US-09-062-113-101	Sequence 101, App
33	103	12.7	981	10	US-09-062-113-92	Sequence 92, Appl
34	103	12.7	984	10	US-09-062-113-93	Sequence 93, Appl
35	103	12.7	1056	10	US-09-062-113-95	Sequence 95, Appl
36	103	12.7	1089	10	US-09-062-113-10	Sequence 10, Appl
37	103	12.7	1182	10	US-09-062-113-100	Sequence 100, App
38	103	12.7	1200	10	US-09-062-113-94	Sequence 94, Appl
39	103	12.7	1203	12	US-10-105-934-3	Sequence 3, Appli
40	103	12.7	1206	10	US-09-062-113-6	Sequence 6, Appli
41	103	12.7	1206	10	US-09-062-113-83	Sequence 83, Appl
42	103	12.7	1206	10	US-09-062-113-84	Sequence 84, Appl
43	103	12.7	1206	10	US-09-062-113-85	Sequence 85, Appl
44	103	12.7	1206	10	US-09-062-113-86	Sequence 86, Appl
45	103	12.7	1206	10	US-09-062-113-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-09-935-727-1
; Sequence 1, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

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;  LOCATION: (25)..(924)
US-09-935-727-1

  Query Match            100.0%;  Score 813;  DB 10;  Length 1077;
  Best Local Similarity  100.0%;  Pred. No. 7.8e-162;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
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Db    172 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 231

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    232 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 291

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 351

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Db    352 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 411

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
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Db    412 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 471

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    472 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 531

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Db    652 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 711

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Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
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Db    772 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 831

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RESULT 2
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; Patent No. US20020061559A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/896,096A
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 2
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: 1090
;   OTHER INFORMATION: Unknown base
US-09-896-096A-2

  Query Match            100.0%;  Score 813;  DB 10;  Length 1114;
  Best Local Similarity  100.0%;  Pred. No. 7.8e-162;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 307

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 427

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 607

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    608 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 667

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    668 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 727

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    728 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 787

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db    788 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 847

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    848 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 907

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    908 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 967

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000


RESULT 3
US-09-894-924-2
; Sequence 2, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/894,924
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 2
;   LENGTH: 1114
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: 1090
;   OTHER INFORMATION: Unknown base
US-09-894-924-2

  Query Match           100.0%;  Score 813;  DB 10;  Length 1114;
  Best Local Similarity  100.0%;  Pred. No. 7.8e-162;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    188 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 247

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 307

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 427

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 607

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    608 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 667

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    668 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 727

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    728 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 787

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    788 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 847

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    848 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 907

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    908 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 967

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||||
Db    968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000


RESULT 4
US-09-877-156-18
; Sequence 18, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
;  APPLICANT: Catherine Tribouley
;  TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE: 1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/877,156
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/286,529
;  PRIOR FILING DATE: 1998-04-05
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
;   LENGTH: 1347
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-877-156-18

  Query Match           100.0%;  Score 813;  DB 10;  Length 1347;
  Best Local Similarity  100.0%;  Pred. No. 8e-162;
  Matches  813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 464

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 524

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    525 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 584

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 644

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 704

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 764

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 824

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 884

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 944

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 1004

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 1064

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 1124

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 1184

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||
Db   1185 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1217


RESULT 5
US-09-840-795-1
; Sequence 1, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Erin E.
;  APPLICANT:  Mattson, Jeanine D.
;  APPLICANT:  Bates, Elizabeth Esther Mary
;  APPLICANT:  Gorman, Daniel M.
;  APPLICANT:  Lebecque, Serge J.E.
;  TITLE OF INVENTION: Mammalian Genes; Related Reagents
;  FILE REFERENCE: SF0818K
;  CURRENT APPLICATION NUMBER: US/09/840,795
;  CURRENT FILING DATE:  2001-04-23
;  PRIOR APPLICATION NUMBER: 09/351,777
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1137
;   TYPE: DNA
;   ORGANISM: primate
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (99)..(998)
;   NAME/KEY: misc_feature
;   LOCATION: (367)
;   OTHER INFORMATION: W; may be A or T
;   NAME/KEY: mat_peptide
;   LOCATION: (132)..(998)
US-09-840-795-1

  Query Match            99.6%;  Score 809.4;  DB 10;  Length 1137;
  Best Local Similarity  99.6%;  Pred. No. 4.4e-161;
  Matches  810;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 245

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    246 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCATGACG 305

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 365

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          |:|||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TWCTGCTACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 425

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 485

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 545

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 605

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 665

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 725

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 785

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 845

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 905

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 965

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          |||||||||||||||||||||||||||||||
Db    966 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 998


RESULT 6
US-09-877-156-19
; Sequence 19, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
;  APPLICANT: Catherine Tribouley
```

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;  TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE: 1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/877,156
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/286,529
;  PRIOR FILING DATE: 1998-04-05
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 1859
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-877-156-19

  Query Match             65.6%;  Score 533.4;  DB 10;  Length 1859;
  Best Local Similarity   98.9%;  Pred. No. 2.6e-103;
  Matches  537;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 224

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     225 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 284

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     285 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 344

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     345 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 404

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     405 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 464

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     465 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 524

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     525 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 584

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     585 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 644

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     645 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCA 704

Qy     541 GAG 543
          |||
Db     705 GAG 707


RESULT 7
US-09-935-727-32
; Sequence 32, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 903
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Mammalian synthetic TNFR-6 alpha
US-09-935-727-32

  Query Match             63.4%;  Score 515.4;  DB 10;  Length 903;
  Best Local Similarity   77.1%;  Pred. No. 1.4e-99;
  Matches  627;  Conservative    0;  Mismatches  186;  Indels    0;  Gaps    0;

Qy       1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
          ||||| |||||||| || || || ||| | || || || ||||| ||  ||||||||||
Db      88 GTGGCTGAAACACCTACATATCCATGGAGAGATGCTGAAACAGGAGAAAGGCTGGTGTGT 147

Qy      61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          || ||||| || || || || ||||||||  |||| ||  | || ||    || ||||||
Db     148 GCTCAGTGTCCTCCTGGAACATTTGTGCAAAGGCCTTGTAGGCGCGATTCTCCTACGACG 207

Qy     121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          |||||||| || || ||  | ||||| || ||||| |||||||| || ||||||| |
Db     208 TGTGGCCCTTGCCCTCCTAGGCACTATACACAGTTTTGGAACTATCTCGAGCGCTGTAGG 267

Qy     181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          || |||||||| ||||| || ||  | || ||||| ||| ||||||| || || || |||
Db     268 TATTGCAACGTGCTCTGTGGAGAAAGGGAAGAGGAAGCAAGGGCTTGTCATGCAACACAC 327

Qy     241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||| | || ||  | || ||||| |||||||| || || ||||| || ||  |||| |||
Db     328 AACAGGGCATGTAGGTGTCGCACAGGCTTCTTTGCTCATGCTGGATTTTGTCTGGAACAC 387

Qy     301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360
          || || ||||| |||||||| || ||||| || || || || |||    |||||||| ||
Db     388 GCTTCTTGTCCTCCTGGTGCTGGAGTGATCGCTCCTGGTACACCCTCTCAGAACACCCAA 447

Qy     361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
          |||||||| || || || ||||||||||| ||    ||||||||||| || || |||||
Db     448 TGCCAGCCCTGTCCTCCTGGCACCTTCTCTGCATCTAGCTCCAGCTCTGAACAATGCCAA 507

Qy     421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
          || |||||||| || || || ||||| ||||| || || ||||| || || |||||||||
Db     508 CCTCACCGCAATTGTACAGCTCTGGGACTGGCTCTGAACGTGCCTGGTTCCTCCTCCCAT 567

Qy     481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
          || || ||||| || ||||| |||||||| || |||   ||| | || || || |||||
Db     568 GATACTCTGTGTACAAGCTGTACTGGCTTTCCTCTCTCACCCGCGTGCCTGGCGCTGAA 627

Qy     541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
          ||||| || || || || |||||||||||||| |||||||| ||||| ||||| ||||||
Db     628 GAGTGCGAACGCGCTGTGATCGACTTTGTGGCCTTCCAGGATATCTCTATCAAAAGGCTG 687
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Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
          || || |||||||| || || || || || ||||||||||||| |||||||||| |||
Db    688 CAACGCCTGCTGCAAGCTCTGGAAGCTCCTGAGGGCTGGGGTCCCACACCAAGGGCTGGC 747

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
           | || ||  |||| |||||||| ||  || ||||||| || |||||||| || || ||
Db    748 AGGGCTGCACTGCAACTGAAGCTTCGCAGGAGGCTCACTGAACTCCTGGGAGCTCAAGAT 807

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
          || || ||||||||| |||||||||| || ||| | ||||| |||||||| || ||||||
Db    808 GGAGCTCTGCTGGTGAGGCTGCTGCAAGCTCTGAGGGTGGCAAGGATGCCTGGACTGGAG 867

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
          ||    ||  | || |||||||| |||||||||
Db    868 CGCTCTGTGAGGGAACGCTTCCTGCCTGTGCAC 900


RESULT 8
US-09-896-096A-3
; Sequence 3, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/896,096A
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
;   LENGTH: 491
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Unknown organism
;   NAME/KEY: unsure
;   LOCATION: 62, 73, 86, 98
;   OTHER INFORMATION: unknown base
US-09-896-096A-3

  Query Match            58.2%;  Score 473.4;  DB 10;  Length 491;
  Best Local Similarity  98.8%;  Pred. No. 7.6e-91;
  Matches  485;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy    101 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGA 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGA 60

Qy    161 ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCAC 220
          | || ||||||| |||||||||||| |||||||||| ||||||||||||||||||||||
Db     61 ANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGGGGAGCGTGAGGAGGAGGCAC 120

Qy    221 GGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACG 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACG 180

Qy    281 CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    181 CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 240

Qy    341 CCCCCAGCCAGAACACGCAGTGCC-AGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC 399
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    241 CCCCCAGCCAGAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC 300

Qy    400 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT 459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT 360

Qy    460 GTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGC 519
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGC 420

Qy    520 ACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAG 579
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAG 480

Qy    580 GACATCTCCAT 590
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Db    481 GACATCTCCAT 491


RESULT 9
US-09-894-924-3
; Sequence 3, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/894,924
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
;   LENGTH: 491
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Unknown organism
;   NAME/KEY: unsure
;   LOCATION: 62, 73, 86, 98
;   OTHER INFORMATION: unknown base
US-09-894-924-3

  Query Match            58.2%;  Score 473.4;  DB 10;  Length 491;
  Best Local Similarity  98.8%;  Pred. No. 7.6e-91;
  Matches  485;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy    101 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGA 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGA 60

Qy    161 ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCAC 220
          | || ||||||| |||||||||||| |||||||||| ||||||||||||||||||||||
Db     61 ANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGGGGAGCGTGAGGAGGAGGCAC 120

Qy    221 GGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACG 280
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Db    121 GGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACG 180

Qy    281 CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 340
Db    181 CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 240

Qy    341 CCCCCAGCCAGAACACGCAGTGCC-AGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC 399
Db    241 CCCCCAGCCAGAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC 300

Qy    400 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT 459
Db    301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT 360

Qy    460 GTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGC 519
Db    361 GTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGC 420

Qy    520 ACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAG 579
Db    421 ACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAG 480

Qy    580 GACATCTCCAT 590
Db    481 GACATCTCCAT 491
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RESULT 10
US-09-877-156-7
; Sequence 7, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 459
; TYPE: DNA
; ORGANISM: human
US-09-877-156-7

Query Match 56.5%; Score 459; DB 10; Length 459;
Best Local Similarity 100.0%; Pred. No. 7.8e-88;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    166 CTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCT 225
Db      1 CTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCT 60

Qy    226 TGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGT 285
Db     61 TGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGT 120

Qy    286 TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC 345
Db    121 TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC 180

Qy    346 AGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGC 405
Db    181 AGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGC 240

Qy    406 TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCA 465
Db    241 TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCA 300

Qy    466 GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGG 525
Db    301 GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGG 360

Qy    526 GTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATC 585
Db    361 GTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATC 420

Qy    586 TCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAG 624
Db    421 TCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAG 459
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RESULT 11
US-09-935-727-33
; Sequence 33, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon optimized TNFR-6 alpha
US-09-935-727-33

Query Match 48.2%; Score 392.2; DB 10; Length 1550;
Best Local Similarity 67.7%; Pred. No. 8.6e-74;
Matches 550; Conservative 0; Mismatches 263; Indels 0; Gaps 0;

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Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60
Db    738 GTTGCTGAAACACCAACTATACCCATGGAGAGATGCTGAAACTGGTGAAAGACTGGTTTGT 797

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
Db    798 GCTCAATGTCCACCAGGTACTTTTGTTCAAAGACCATGTAGAAGAGATTCTCCAACTACT 857

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
Db    858 TGTGGTCCATGTCCACCAAGACATTACACTCAATTTTGGAACTACCTGGAAAGATGTAGA 917

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
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Db    918 TACTGTAACGTTCTTTGTGGTGAAAGAGAAGAAGAAGCTAGAGCTTGTCATGCTACTCAT 977

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Db    978 AACAGAGCTTGTAGATGTAGAACTGGTTTTTTTGCTCATGCTGGTTTTTGTTTGGAACAT 1037

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Db   1038 GCTTCTTGTCCACCTGGTGCTGGTGTTATTGCTCCTGGTACTCCTTCTCAAAACACTCAA 1097

Qy    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Db   1098 TGTCAGCCATGTCCACCAGGTACTTTTTCTGCTTCTTCTTCTTCTTCTGAACAATGTCAA 1157

Qy    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Db   1158 CCACATAGAAACTGTACTGCTTTGGGTCTGGCTTTGAATGTTCCAGGTTCTTCTTCTCAT 1217

Qy    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Db   1218 GATACTTTGTGTACTTCTTGTACTGGTTTTCCTTTGTCTACTAGAGTTCCAGGTGCTGAA 1277

Qy    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Db   1278 GAATGTGAAAGAGCTGTTATTGATTTTGTTGCTTTTCAAGATATTTCTATTAAGAGACTG 1337

Qy    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Db   1338 CAAAGACTGCTGCAAGCTCTGGAAGCTCCAGAAGGTTGGGGTCCAACTCCAAGAGCTGGT 1397

Qy    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Db   1398 AGAGCTGCTTTGCAATTGAAGTTGAGAAGAAGATTGACAGAATTGTTGGGTGCTCAAGAT 1457

Qy    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Db   1458 GGTGCTTTGTTGGTTAGATTGTTGCAAGCTTTGAGAGTTGCTAGAATGCCTGGTTTGGAA 1517

Qy    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813

Db   1518 AGATCTGTTAGAGAAAGATTTTTGCCAGTTCAC 1550
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RESULT 12
US-09-935-727-3
; Sequence 3, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)..(582)
US-09-935-727-3

Query Match 47.7%; Score 387.4; DB 10; Length 1667;
Best Local Similarity 79.6%; Pred. No. 8.8e-73;
Matches 534; Conservative 0; Mismatches 1; Indels 136; Gaps 1;

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Qy      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Db    160 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 219

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Db    220 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 279

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Db    280 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 339

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Db    340 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 399

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Db    400 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 459

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCG---------------------------- 336

Db    460 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGG 519

Qy    337 ------------------------------------------------------------ 336

Db    520 GCCCCCAGGAGTGGTGGCCGGAGGTGTGGCAGGGGTCAGGTTGCTGGTCCCAGCCTTGCA 579

Qy    337 ----------------------------------------------------------GGCACCCC 344

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Qy    525 GGTACCAGGAG 535

Db    820 GGTACCAGGTG 830
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RESULT 13
US-09-935-727-28
; Sequence 28, Application US/09935727
; Patent No. US20020150583A1

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; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 1796
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 425-560
;   NAME/KEY: intron
;   LOCATION: 756-1512
US-09-935-727-28

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  Best Local Similarity  79.4%;  Pred. No. 1.1e-72;
  Matches  533;  Conservative    1;  Mismatches    1;  Indels  136;  Gaps    1;

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Db     88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
          ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db    208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTRGAGCGCTGCCGC 267

Qy    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCG---------------------- 336
          |||||||||||||||||||||||||||||||||
Db    388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGG 447

Qy    337 ---------------------------------------------------------- 336
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Db    448 GCCCCCAGGAGTGGTGGCCGGAGGTGTGGCAGGGGTCAGGTTGCTGGTCCCAGCCTTGCA 507

Qy    337 ----------------------------------------------------GGCACCCC 344
                                                                 ||||||||
Db    508 CCCTGAGCTAGGACACCAGTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCC 567

Qy    345 CAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAG 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 CAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAG 627

Qy    405 CTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCC 464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 CTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCC 687

Qy    465 AGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAG 524
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 AGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAG 747

Qy    525 GGTACCAGGAG 535
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Db    748 GGTACCAGGTG 758


RESULT 14
US-09-896-096A-5
; Sequence 5, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/896,096A
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 5
;   LENGTH: 271
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Unknown organism
;   NAME/KEY: unsure
;   LOCATION: 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233
;   OTHER INFORMATION: unknown base
US-09-896-096A-5

  Query Match            30.2%;  Score 245.2;  DB 10;  Length 271;
  Best Local Similarity  92.3%;  Pred. No. 3.8e-43;
  Matches  250;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy    101 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGA 160
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Db      1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACGCAGTTCTGGA 60

Qy    161 ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCAC 220
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Qy    221 GGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACG 280
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Qy    281 CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 340
          ||| |||||||||||||||||||||||||||||||||| |||||||||||| |||||||
Db    181 CTGNTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCA 240

Qy    341 CCCCCAGCCAGAACACGCAGTGCCAGCCGTG 371
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Db    241 CCCCCAGCCAGAACACGCATGCAAAGCCGTG 271


RESULT 15
US-09-894-924-5
; Sequence 5, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/894,924
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 5
;   LENGTH: 271
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Unknown organism
;   NAME/KEY: unsure
;   LOCATION: 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233
;   OTHER INFORMATION: unknown base
US-09-894-924-5

  Query Match             30.2%;  Score 245.2;  DB 10;  Length 271;
  Best Local Similarity   92.3%;  Pred. No. 3.8e-43;
  Matches  250;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy    101 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGA 160
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db      1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACGCAGTTCTGGA 60

Qy    161 ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCAC 220
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Qy    221 GGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACG 280
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Db    181 CTGNTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCA 240

Qy    341 CCCCCAGCCAGAACACGCAGTGCCAGCCGTG 371
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Db    241 CCCCCAGCCAGAACACGCATGCAAAGCCGTG 271
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Search completed: January 6, 2003, 16:08:07
Job time : 63 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2003, 11:21:41 ; Search time 2905 Seconds
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2714.926 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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21	1476	99.0	936	6	AX167230	AX167230 Sequence
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27	499.5	33.5	1148	5	OMY315137	AJ315137 Oncorhync
28	486.5	32.6	1116	5	AF401631	AF401631 Oncorhync
29	440.5	29.5	1156	9	AF134187	AF134187 Homo sapi
30	440.5	29.5	1206	6	E15271	E15271 Human mRNA
31	440.5	29.5	1206	9	AB002146	AB002146 Homo sapi
32	440.5	29.5	1355	6	AR168730	AR168730 Sequence
33	440.5	29.5	1355	6	AR205589	AR205589 Sequence
34	440.5	29.5	1356	6	AX333682	AX333682 Sequence
35	440.5	29.5	1356	9	HSU94332	U94332 Human osteo
36	440.5	29.5	1719	9	BC030155	BC030155 Homo sapi
37	440.5	29.5	2139	6	AX202074	AX202074 Sequence
38	436.5	29.3	1356	6	AX076608	AX076608 Sequence
39	433	29.0	525	6	AR099131	AR099131 Sequence
40	425.5	28.5	2432	6	AR168728	AR168728 Sequence
41	425.5	28.5	2432	6	AR205587	AR205587 Sequence
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43	424.5	28.5	1324	6	AR168729	AR168729 Sequence
44	424.5	28.5	1324	6	AR205588	AR205588 Sequence
45	424.5	28.5	1325	10	MMU94331	U94331 Mus musculu

ALIGNMENTS

RESULT 1

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DEFINITION  Sequence 2 from Patent WO0128582.
ACCESSION   AX119833
VERSION     AX119833.1  GI:14036593
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 813)
  AUTHORS   Bumol,T.F. and Cohen,F.J.
  TITLE     Therapeutic applications of flint polypeptides
  JOURNAL   Patent: WO 0128582-A 2 26-APR-2001;
            ELI LILLY AND COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .813
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BASE COUNT      122 a    298 c    267 g    126 t
ORIGIN

Alignment Scores:
Pred. No.:              3.84e-64        Length:         813
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-936-024-1 (1-271) x AX119833 (1-813)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

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Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
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Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813

RESULT 2
AX167223
LOCUS       AX167223                813 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 2 from Patent WO0142463.
ACCESSION   AX167223
VERSION     AX167223.1  GI:14596692
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 813)
  AUTHORS   Lu,J. and Witcher,D.R.
  TITLE     Improving stability of flint through o-linked glycosylation
  JOURNAL   Patent: WO 0142463-A 2 14-JUN-2001;
            ELI LILLY AND COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .813
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      122 a    298 c    267 g    126 t
ORIGIN

Alignment Scores:
Pred. No.:              3.84e-64        Length:         813
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-936-024-1 (1-271) x AX167223 (1-813)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db      1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 60

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160

Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180

Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200

Db    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220

Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240

Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260

Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271

Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813

RESULT 3
AX375169
LOCUS       AX375169                813 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 2 from Patent WO0209668.
ACCESSION   AX375169
VERSION     AX375169.1  GI:19169920
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Micanovic,R. and Witcher,D.R.
  TITLE     Pulmonary administration of flint
  JOURNAL   Patent: WO 0209668-A 2 07-FEB-2002;
            ELI LILLY AND COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .813
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      122 a    298 c    267 g    126 t
ORIGIN

Alignment Scores:
Pred. No.:              3.84e-64        Length:         813
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-936-024-1 (1-271) x AX375169 (1-813)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20

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Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40

Db     61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 120

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60

Db    121 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80

Db    181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 240

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100

Db    241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120

Db    301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 360

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140

Db    361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160

Db    421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180

Db    481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200

Db    541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220

Db    601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240

Db    661 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260

Db    721 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271

Db    781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813

RESULT 4
AF134240
LOCUS       AF134240                903 bp    mRNA    linear   PRI 11-MAY-1999
DEFINITION  Homo sapiens tumor necrosis factor receptor homolog (TR6) mRNA,
            complete cds.
ACCESSION   AF134240
VERSION     AF134240.1  GI:4768938
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   Yu,K.Y., Kwon,B., Ni,J., Zhai,Y., Ebner,R. and Kwon,B.S.
  TITLE     A newly identified member of tumor necrosis factor receptor
            superfamily (TR6) suppresses LIGHT-mediated apoptosis
  JOURNAL   J. Biol. Chem. 274 (20), 13733-13736 (1999)
  MEDLINE   99253915
   PUBMED   10318773
REFERENCE   2  (bases 1 to 903)
  AUTHORS   Kwon,B.S. and Yu,K.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAR-1999) Micro/Immunol, Indiana University, 635
            Barnhill Drive, Indianapolis, IN 46202, USA
FEATURES             Location/Qualifiers
     source          1. .903
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     CDS             1. .903
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                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
                     VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      129 a    324 c    305 g    145 t
ORIGIN

Alignment Scores:
Pred. No.:              4.27e-64        Length:         903
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-936-024-1 (1-271) x AF134240 (1-903)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db     88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 207

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    208 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 267

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db    268 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 327

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 447

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
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Db    448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 507

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 567

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 627

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Db    628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 747

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db    748 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 807

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db    808 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 867

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db    868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900

RESULT 5
AF217794
LOCUS       AF217794                1048 bp    mRNA    linear   PRI 12-FEB-2000
DEFINITION  Homo sapiens M68E mRNA, alternatively spliced, complete cds.
ACCESSION   AF217794
VERSION     AF217794.1  GI:6969262
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1048)
  AUTHORS   Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
            Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
            Caskey,C.T.
  TITLE     Overexpression of M68/DcR3 in human gastrointestinal tract tumors
            independent of gene amplification and its location in a four-gene
            cluster
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
  MEDLINE   20122600
   PUBMED   10655513
REFERENCE   2  (bases 1 to 1048)
  AUTHORS   Bai,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,
            Sumneytown Pike, West Point, PA 19403, USA
FEATURES             Location/Qualifiers
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                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      160 a    367 c    335 g    186 t
ORIGIN

Alignment Scores:
Pred. No.:              4.97e-64        Length:         1048
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-936-024-1 (1-271) x AF217794 (1-1048)
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Db     140 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 199

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 259

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db     260 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 319

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db     320 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 379

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db     380 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 439

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db     440 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 499

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
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Db     560 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 619

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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Db     620 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 679

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db     800 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 859

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db     860 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 919

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
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Db     920 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 952
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RESULT 6
AX082868
LOCUS       AX082868               1055 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 1 from Patent WO0110908.
ACCESSION   AX082868
VERSION     AX082868.1  GI:13184802
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1055)
  AUTHORS   Hsu,H.
  TITLE     Ntr3, a member of the tnf-receptor supergene family
  JOURNAL   Patent: WO 0110908-A 1 15-FEB-2001;
            Amgen Inc. (US)
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                     /db_xref="GI:13184803"
                     /translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
                     ERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEA
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                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
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                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      160 a    369 c    340 g    186 t
ORIGIN
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Alignment Scores:
Pred. No.:                5e-64          Length:          1055
Score:                    1491.00        Matches:         271
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-936-024-1 (1-271) x AX082868 (1-1055)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db     154 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 213

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 273

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 333

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 393

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 453

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db     454 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 513

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 573

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 633

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 693

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 753

Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 813

Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 873

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db    874 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 933

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db    934 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 966

RESULT 7
AX055373
LOCUS       AX055373               1114 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 3 from Patent WO0073452.
ACCESSION   AX055373
VERSION     AX055373.1  GI:12228659
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1114)
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
            Tumas,D., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 0073452-A 3 07-DEC-2000;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1114
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      188 a    379 c    356 g    191 t
ORIGIN

Alignment Scores:
Pred. No.:                5.28e-64        Length:         1114
Score:                    1491.00         Matches:        271
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       6               Gaps:           0

US-09-936-024-1 (1-271) x AX055373 (1-1114)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db    188 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 247

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 307

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    308 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db    368 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 427

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Db    548 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 607

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
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Db    608 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 667

Qy    161 AspThrLeuCysThrSerCysThrGlyProLeuSerThrArgValProGlyAlaGlu 180
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Db    668 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 727

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Db    728 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 787

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db    788 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 847

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db    848 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 907

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db    908 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 967

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
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Db    968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000

RESULT 8
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LOCUS       AX056645               1114 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 1 from Patent WO0075316.
ACCESSION   AX056645
VERSION     AX056645.1  GI:12309639
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1114)
  AUTHORS   Ashkenazi,A.J., Goddard,A., Gurney,A.L., Hillan,K., Napier,M. and
            Wood,W.I.
  TITLE     Methods and compositions for inhibiting neoplastic cell growth
  JOURNAL   Patent: WO 0075316-A 1 14-DEC-2000;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1114
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      188 a    379 c    356 g    191 t
ORIGIN

Alignment Scores:
Pred. No.:                5.28e-64        Length:         1114
Score:                    1491.00         Matches:        271
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       6               Gaps:           0

US-09-936-024-1 (1-271) x AX056645 (1-1114)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    308 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

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Db    368 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 427

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100

Db    428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120

Db    488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140

Db    548 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 607

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160

Db    608 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 667

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180

Db    668 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 727

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200

Db    728 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 787

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220

Db    788 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 847

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240

Db    848 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 907

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260

Db    908 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 967

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271

Db    968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000
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RESULT 9
AF104419
LOCUS       AF104419                1114 bp    mRNA    linear   PRI 06-JAN-1999
DEFINITION  Homo sapiens decoy receptor 3 (DcR3) mRNA, complete cds.
ACCESSION   AF104419
VERSION     AF104419.1  GI:4106877
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1114)
  AUTHORS   Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
            Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
            Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
            Goddard,A.D., Botstein,D. and Ashkenazi,A.
  TITLE     Genomic amplification of a decoy receptor for Fas ligand in lung
            and colon cancer
  JOURNAL   Nature 396 (6712), 699-703 (1998)
  MEDLINE   99087326
   PUBMED   9872321
REFERENCE   2  (bases 1 to 1114)
  AUTHORS   Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
            Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
            Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
            Goddard,A.D., Botstein,D. and Ashkenazi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way,
            San Francisco, CA 94080, USA
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                     /chromosome="20"
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                     /note="linked by radiation-hybrid analysis to chromosome
                     20 marker AFM218xe7"
     gene            1. .1114
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     CDS             101. .1003
                     /gene="DcR3"
                     /function="binds to Fas/Apo1/CD95 ligand and blocks its
                     activity"
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                     factor receptor family; amplified in lung and colon
                     cancer"
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                     /product="decoy receptor 3"
                     /protein_id="AAD03056.1"
                     /db_xref="GI:4106878"
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                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
                     VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      188 a    379 c    356 g    191 t
ORIGIN
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Alignment Scores:
Pred. No.:              5.28e-64        Length:         1114
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-936-024-1 (1-271) x AF104419 (1-1114)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20

Db    188 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 247

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40

Db    248 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 307

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60

Db    308 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80

Db    368 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 427

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100

Db    428 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 487

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120

Db    488 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 547

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140

Db    548 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 607

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
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Db    608 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 667

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    668 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 727

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    728 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 787

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db    788 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 847

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    848 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 907

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db    908 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 967

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          ||||||||||||||||||||||||||||||||
Db    968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000

RESULT 10
BC017065
LOCUS       BC017065                1125 bp    mRNA    linear   PRI 09-NOV-2001
DEFINITION  Homo sapiens, tumor necrosis factor receptor superfamily, member
            6b, decoy, clone MGC:9587 IMAGE:3886635, mRNA, complete cds.
ACCESSION   BC017065
VERSION     BC017065.1  GI:16877637
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1125)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 22 Row: d Column: 23
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 14790166.
FEATURES             Location/Qualifiers
     source          1. .1125
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                     /db_xref="LocusID:8771"
                     /db_xref="taxon:9606"
                     /clone="MGC:9587 IMAGE:3886635"
                     /tissue_type="Lung, carcinoma, large cell
                     undifferentiated."
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                     /lab_host="DH10B"
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                     /codon_start=1
                     /product="tumor necrosis factor receptor superfamily,
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                     /protein_id="AAH17065.1"
                     /db_xref="GI:16877638"
                     /translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
                     ERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEA
                     RACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA
                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
                     VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      200 a    378 c    356 g    191 t
ORIGIN

Alignment Scores:
Pred. No.:              5.34e-64        Length:         1125
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-936-024-1 (1-271) x BC017065 (1-1125)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db    187 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 246

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 306

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 366

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 426

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    427 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 486

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db    487 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 546

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 606

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 666

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 726

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 786

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db    787 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 846

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 906
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Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db    907 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 966

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db    967 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 999

RESULT 11
BC034349
LOCUS       BC034349               1150 bp    mRNA    linear   PRI 08-JUL-2002
DEFINITION  Homo sapiens, tumor necrosis factor receptor superfamily, member
            6b, decoy, clone MGC:21079 IMAGE:4752507, mRNA, complete cds.
ACCESSION   BC034349
VERSION     BC034349.1  GI:21706464
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
            Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
            Richards, S., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 28 Row: o Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 14790166.
FEATURES              Location/Qualifiers
     source           1. .1150
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                      /db_xref="taxon:9606"
                      /clone="MGC:21079 IMAGE:4752507"
                      /tissue_type="Skin, squamous cell carcinoma"
                      /clone_lib="NCI_CGAP_Skn4"
                      /lab_host="DH10B"
                      /note="Vector: pCMV-SPORT6.ccdb"
     CDS              109. .1011
                      /codon_start=1
                      /product="tumor necrosis factor receptor superfamily,
                      member 6b, decoy"
                      /protein_id="AAH34349.1"
                      /db_xref="GI:21706465"
                      /db_xref="LocusID:8771"
                      /translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
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                      RACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA
                      SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
                      VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
                      LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      222 a    382 c    348 g    198 t
ORIGIN
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Alignment Scores:
Pred. No.:                5.46e-64        Length:          1150
Score:                    1491.00         Matches:         271
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       9               Gaps:            0

US-09-936-024-1 (1-271) x BC034349 (1-1150)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db    196 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 255

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Db    256 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 315

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    316 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTAGAGCGCTGCCGC 375

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db    376 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 435

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 495

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 555

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 615

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    616 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 675

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 735

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Db    736 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 795

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db    796 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 855

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db    856 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 915

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db    916 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 975

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
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Db    976 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1008

RESULT 12
AX017828
LOCUS       AX017828               1168 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9946376.
ACCESSION   AX017828
VERSION     AX017828.1  GI:10042431
KEYWORDS    .
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SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1168)
  AUTHORS   Kroeger,B.
  TITLE     Receptor from the superfamily of tnt-receptors from the human lung
  JOURNAL   Patent: WO 9946376-A 1 16-SEP-1999;
            BASF AG (DE); KROEGER BURKHARD (DE)
FEATURES             Location/Qualifiers
     source          1. .1168
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             134. .1036
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC07698.1"
                     /db_xref="GI:10042432"
                     /translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
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                     RACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA
                     SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
                     VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
                     LQALRVARMPGLERSVRERFLPVH"
BASE COUNT      194 a    392 c    371 g    211 t
ORIGIN

Alignment Scores:
Pred. No.:              5.54e-64        Length:         1168
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-936-024-1 (1-271) x AX017828 (1-1168)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 280

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 340

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 400

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 460

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    461 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 520

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db    521 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 580

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Db    581 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 640

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    641 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 700

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    701 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 760

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    761 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 820

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    821 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 880

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db    881 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 940

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db    941 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 1000

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
          |||||||||||||||||||||||||||||||
Db   1001 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1033

RESULT 13
AR171895
LOCUS       AR171895               1347 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 18 from patent US 6297367.
ACCESSION   AR171895
VERSION     AR171895.1  GI:17910845
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1347)
  AUTHORS   Tribouley,C.
  TITLE     Polynucleotide encoding TNFL1
  JOURNAL   Patent: US 6297367-A 18 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1347
                     /organism="unknown"
BASE COUNT      230 a    444 c    443 g    230 t
ORIGIN

Alignment Scores:
Pred. No.:              6.4e-64         Length:         1347
Score:                  1491.00         Matches:        271
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-936-024-1 (1-271) x AR171895 (1-1347)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db    405 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 464

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Db    465 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 524

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    525 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 584

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db    585 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 644

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    645 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 704

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 764
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Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Db    765 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 824

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 884

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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Db    885 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 944

Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Db    945 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 1004

Qy    201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db   1005 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 1064

Qy    221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db   1065 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 1124

Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db   1125 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 1184

Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
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Db   1185 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1217

RESULT 14
AF217793
LOCUS       AF217793               1428 bp    mRNA    linear   PRI 12-FEB-2000
DEFINITION  Homo sapiens M68C mRNA, alternatively spliced, complete cds.
ACCESSION   AF217793
VERSION     AF217793.1  GI:6969260
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1428)
  AUTHORS   Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
            Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
            Caskey,C.T.
  TITLE     Overexpression of M68/DcR3 in human gastrointestinal tract tumors
            independent of gene amplification and its location in a four-gene
            cluster
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
  MEDLINE   20122600
   PUBMED   10655513
REFERENCE   2  (bases 1 to 1428)
  AUTHORS   Bai,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,
            Sumneytown Pike, West Point, PA 19403, USA
FEATURES             Location/Qualifiers
     source          1. .1428
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BASE COUNT      240 a    500 c    448 g    240 t
ORIGIN

Alignment Scores:
Pred. No.:                6.79e-64        Length:          1428
Score:                    1491.00         Matches:         271
Percent Similarity:       100.00%         Conservative:    0
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Query Match:              100.00%         Indels:          0
DB:                       9               Gaps:            0

US-09-936-024-1 (1-271) x AF217793 (1-1428)

Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    522 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 581

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Db    582 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 641

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    642 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 701

Qy     61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    762 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 821

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
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Db    942 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 1001

Qy    161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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Qy    181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Qy    241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Qy    261 ArgSerValArgGluArgPheLeuProValHis 271
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RESULT 15
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LOCUS       AB029011                4945 bp    mRNA    linear   PRI 10-MAY-2002
DEFINITION  Homo sapiens mRNA for KIAA1088 protein, partial cds.
ACCESSION   AB029011
VERSION     AB029011.2  GI:20521759
KEYWORDS    .
SOURCE      Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
            clone:hk02589s1.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kikuno,R., Nagase,T., Ishikawa,K., Hirosawa,M., Miyajima,N.,
            Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XIV. The complete sequences of 100 new cDNA clones from brain which
            code for large proteins in vitro
  JOURNAL   DNA Res. 6 (3), 197-205 (1999)
  MEDLINE   99397452
   PUBMED   10470851
REFERENCE   2  (bases 1 to 4945)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute,
            Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
COMMENT     On May 9, 2002 this sequence version replaced gi:5689512.
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BASE COUNT      963 a   1581 c   1529 g    872 t
ORIGIN

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Score:                    1491.00         Matches:         271
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       9               Gaps:            0

US-09-936-024-1 (1-271) x AB029011 (1-4945)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3995 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 4054

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Db    4055 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 4114

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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Db    4175 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 4234

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    4235 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 4294

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db    4295 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 4354

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
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Db    4355 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 4414

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
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Db    4415 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 4474

Qy     161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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Db    4475 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 4534

Qy     181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Qy     201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Qy     221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Db    4655 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 4714

Qy     241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db    4715 GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 4774

Qy     261 ArgSerValArgGluArgPheLeuProValHis 271
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Job time : 2909 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:33 ; Search time 73 Seconds
(without alignments)
764.915 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	499.5	33.5	285	13	Q90W71	Q90w71 oncorhynchu
2	486.5	32.6	285	13	Q90YS6	Q90ys6 oncorhynchu
3	395	26.5	302	13	Q9PUS0	Q9pus0 salvelinus
4	333.5	22.4	459	11	Q62327	Q62327 mus musculu
5	327	21.9	482	11	O88734	O88734 mus musculu
6	313.5	21.0	433	11	Q91ZM6	Q91zm6 rattus norv
7	287	19.2	651	13	Q98SM6	Q98sm6 gallus gall
8	275	18.4	348	12	O57103	O57103 monkeypox v
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18	260	17.4	349	12	O57110	O57110 variola vir
19	260	17.4	349	12	O57111	O57111 variola vir
20	260	17.4	349	12	Q89098	Q89098 variola vir
21	260	17.4	349	12	Q89118	Q89118 variola vir
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23	259	17.4	360	12	O57118	O57118 cowpox viru
24	258.5	17.3	355	12	Q85308	Q85308 cowpox viru
25	257.5	17.3	326	12	O57120	O57120 cowpox viru
26	257.5	17.3	349	12	O57098	O57098 camelpox vi
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28	257.5	17.3	349	12	O57284	O57284 camelpox vi
29	254.5	17.1	326	12	O57122	O57122 cowpox viru
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31	253.5	17.0	349	12	O57097	O57097 camelpox vi
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33	253.5	17.0	351	12	O57117	O57117 cowpox viru
34	252	16.9	349	12	O57109	O57109 variola vir
35	251	16.8	347	12	O57119	O57119 cowpox viru
36	249.5	16.7	347	12	O57115	O57115 cowpox viru
37	248.5	16.7	351	12	O57121	O57121 cowpox viru
38	245.5	16.5	350	12	O57123	O57123 cowpox viru
39	244	16.4	283	6	Q9XSZ8	Q9xsz8 cercopithec
40	230.5	15.5	276	13	Q9DDD2	Q9ddd2 gallus gall
41	227	15.2	278	6	Q8SQ34	Q8sq34 sus scrofa
42	219.5	14.7	277	6	Q8WMQ2	Q8wmq2 ovis aries
43	203.5	13.6	267	6	O02764	O02764 oryctolagus
44	202	13.5	132	13	Q90Y18	Q90y18 salvelinus
45	200	13.4	167	12	Q9DJL2	Q9djl2 cowpox viru

ALIGNMENTS

RESULT 1
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AC Q90W71;
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEAD KIDNEY;
RA Pleguezuelos O., Secombes C.J.;
RT "Screening a rainbow trout (Oncorhynchus mykiss) cDNA library.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ315137; CAC43329.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;

Query Match 33.5%; Score 499.5; DB 13; Length 285;
Best Local Similarity 37.1%; Pred. No. 5e-36;
Matches 99; Conservative 41; Mismatches 116; Indels 11; Gaps 4;

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Qy      2 AETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRY 61
          | |||| |||  ||: | |  | |||:: : | :|  : |||||  |||: |||:|||:|
Db     26 AHTPTYIWRDDATGDSLTCDLCAPGTYLLKHCTKDRKSDCGPCPKSHYTEIWNYIERCQY 85

Qy     62 CNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQC 121
            ||  |   | |:  |   ||| | |: ||:   | |  |  |||| |||: ||   : :|
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Db     86 CNRFCTADEIESVPCTQLHNRQCECKDGFYMTHGSCSRHRRCPPGEGVISNGTAHTDVKC 145

Qy    122 QPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE 181
          :||| | ||| ||| : ||    |   |    :||:  :|  |::||    |    |
Db    146 EPCPVGFFSAVSSSRKACQKFSVCPPGG--TTIPGNDMNDVYCSACTNG--SRTHEGEAI 201

Qy    182 CERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDG 241
          |:  :::|:: | :: :: :||:  |    |   |       | | | : :    |
Db    202 CDGELMEFLSLQILTPRKDKRLVAVLRRSAGKATT----NNATVLDLLKTIKNKAGKH-- 255

Qy    242 ALLVRLLQALRVARMPGLERSVRERFL 268
             :::   |   |:  |   | : ||
Db    256 -FAIQMRDILNTDRLLHLRTKVNKWFL 281


RESULT 2
Q90YS6
ID   Q90YS6      PRELIMINARY;      PRT;   285 AA.
AC   Q90YS6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TNF decoy receptor.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu L., Fujiki K., Dixon B., Sundick R.S.;
RT   "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
RT   with a fractalkine-like stalk and a TNF decoy receptor using cDNA
RT   fragments containing AU-rich elements.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF401631; AAK91758.1; -.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00181; EGF; 1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   285 AA;  31795 MW;  5E3BD1B6EFC6BABC CRC64;

  Query Match           32.6%;  Score 486.5;  DB 13;  Length 285;
  Best Local Similarity  36.3%;  Pred. No. 6.9e-35;
  Matches   97;  Conservative   41;  Mismatches  118;  Indels   11;  Gaps    4;

Qy      2 AETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRY 61
          | |||| ||| ||: | |  | ||| :: : | :|  : |||||  |||: |||:|||:|
Db     26 AHTPTYIWRDDATGDSLTCDLCAPGTYLLKHCTKDRKSDCGPCPKSHYTEIWNYIERCQY 85

Qy     62 CNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQC 121
          ||  |   | |:  |   ||| | |: ||:   | |  |  |||| |||: ||   : :|
Db     86 CNRFCTADEIESVPCTQLHNRQCECKDGFYMTHGSCSRHRRCPPGEGVISNGTAHTDVKC 145

Qy    122 QPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE 181
          :||| | ||| ||| : ||     |         :||:  :|  |::|     |    |
Db    146 EPCPVGFFSAVSSSRKACQKFSVCPP--GRTTIPGNDMNDVYCSACRNG--SRTHEGQAI 201

Qy    182 CERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDG 241
          |:  :::|:: | :: :: :||:  |    |   |       | | | : :    |
Db    202 CDGELMEFLSLQILTPRKDKRLVAVLRRSAGKATT----NNATVLDLLKTIKNKAGKH-- 255

Qy    242 ALLVRLLQALRVARMPGLERSVRERFL 268
             :::   |   |:  |   | : ||
Db    256 -FAIQMRDILNTDRLLHLRTKVNKWFL 281


RESULT 3
Q9PUS0
ID   Q9PUS0      PRELIMINARY;      PRT;   302 AA.
AC   Q9PUS0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Decoy TNF receptor.
OS   Salvelinus fontinalis (Brook trout) (Brook char).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX   NCBI_TaxID=8038;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20111091; PubMed=10642582;
RA   Bobe J., Goetz F.W.;
RT   "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT   the brook trout (Salvelinus fontinalis) ovary at the completion of
RT   ovulation.";
RL   Biol. Reprod. 62:420-426(2000).
DR   EMBL; AF156738; AAD56428.1; -.
DR   HSSP; O14763; 1D4V.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   302 AA;  34037 MW;  E44C73477F05C3DF CRC64;

  Query Match           26.5%;  Score 395;  DB 13;  Length 302;
  Best Local Similarity  34.3%;  Pred. No. 7.7e-27;
  Matches   82;  Conservative   44;  Mismatches  101;  Indels   12;  Gaps    7;

Qy      6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 65
          |:   | :|  :|| :|||||::: ||     : |  ||   ||:|||:: :|  |: :
Db     22 TFKNDDRYSGLSIVCDRCPPGTYLRAPCSAMRKSDCAECPNGAYTEFWNHISKCLRCS-M 80

Qy     66 CGEREEEARACHATHNRACRCRTGFFAHAGF--CLEHASCPPGAGVIAPGTPSQNTQCQP 123
          | | :   : |  ::|  | |: |:: :  :  |::|  |||| |    ||| |:|:|
Db     81 CAENQVVKQECSPSNNCECECKEGYYFNKKYEACIKHKECPPGYGANTTGTPHQDTECVQ 140

Qy    124 CPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECE 183
          |  | :|  ||:   |    ||   || : : |   |:||| ||  : | ||  |||
Db    141 CQAGFYSEVSSAKATCLAQSNCKVGGLRVVLKGQDWHNTLCASC--YDLKTR-DGAEYLH 197

Qy    184 RAVIDFV--AFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
            :  |     | :.|||::||  |:  |:  |  |  |  |:  : || | : : : |
Db    198 EILPTFFIQLHQTMGIKRMRRL--AMRLPQEGGKKPLIG--AVMKRNRRGLHDFMNSWD 252


RESULT 4
Q62327
ID   Q62327      PRELIMINARY;      PRT;   459 AA.
AC   Q62327;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Murine tumour necrosis factor receptor 2 protein (Fragment).
GN   TNFRSF1B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD;
RA   Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT   "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT   linked to autoimmune diabetes in NOD mice.";
RL   Genomics 0:0-0(0).
RN   [2]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD;
RX   MEDLINE=95178848; PubMed=7873884;
RA   Powell B.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT   "Allelic variation of the type 2 tumor necrosis factor receptor
RT   gene.";
RL   Mamm. Genome 5:726-727(1994).
DR   EMBL; X76401; CAA53981.1; -.
DR   HSSP; P19438; 1NCF.
DR   MGD; MGI:1314883; Tnfrsf1b.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER       1      1
FT   VARIANT      87     87       S -> T.
FT   VARIANT      93     93       T -> I.
FT   VARIANT     268    268       F -> I.
FT   VARIANT     345    345       S -> F.
FT   VARIANT     421    421       Y -> C.
SQ   SEQUENCE   459 AA;  48686 MW;  6C51D2CF1C4626DF CRC64;

  Query Match             22.4%;  Score 333.5;  DB 11;  Length 459;
  Best Local Similarity   29.7%;  Pred. No. 3e-21;
  Matches   81;  Conservative   43;  Mismatches  110;  Indels   39;  Gaps    9;

Qy      17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
           :: ||:|||| :|:  | : | | |  |    ||| ||    |  |: |   : | |||
Db      37 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRAC 96

Qy      77 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
              || | |  | :     |:|    |:  : | || || :   |: |  |: | ||||
Db      97 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 156

Qy     130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
           | ::||:: |:||| |: |     :||::| | :|     : :  | :  |    |
Db     157 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 212

Qy     186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 240
            :|    |:    :   :| :|       | ||       |  :| : |   :| |
Db     213 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 257

Qy     241 GALLVRLLQAL----RVARMPGLERSVRERFLP 269
           | |:: |:       |  :   |:|  :   :|
Db     258 GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP 290


RESULT 5
O88734
ID   O88734      PRELIMINARY;      PRT;   482 AA.
AC   O88734;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   P80 TNF-alpha receptor.
GN   TNFR2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98414512; PubMed=9740674;
RA   Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT   "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
RT   and Characterization of the two Transcripts.";
RL   Genomics 52:79-98(1998).
DR   EMBL; Y14619; CAA74969.1; -.
DR   EMBL; Y14620; CAA74969.1; JOINED.
DR   EMBL; Y14621; CAA74969.1; JOINED.
DR   EMBL; Y14622; CAA74969.1; JOINED.
DR   EMBL; Y14623; CAA74969.1; JOINED.
DR   EMBL; Y14679; CAA74969.1; JOINED.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
SQ   SEQUENCE   482 AA;  51106 MW;  F6C15046B48FF83C CRC64;

  Query Match             21.9%;  Score 327;  DB 11;  Length 482;
  Best Local Similarity   29.3%;  Pred. No. 1.2e-20;
  Matches   82;  Conservative   43;  Mismatches  109;  Indels   46;  Gaps   10;

Qy      17 RLVCAQCPPGTFVQRPCRR-------DSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGER 69
           :: ||:|||| :|:  | :       || | |  |    ||| ||    |  |: |
Db      52 QMCCAKCPPGQYVKHFCNKTSDTVCADSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTD 111

Qy      70 EEEARACHATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQ 122
           : | |||    || | |  | :     |:|    |:  : | || || :   |: | |:
Db     112 QVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCK 171

Qy     123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPG 178
           | |||| ::||:: |:||| |: |     :||::| | :|     : :  | :  |
Db     172 ACAPGTFSDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQ 227

Qy     179 AEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLT 233
           |     :|    |:    :   :| :|       | ||       |  :| : |   :|
Db     228 PEPTRSQPLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVT 277

Qy     234 ELLGAQDGALLVRLLQAL----RVARMPGLERSVRERFLP 269
           |     | |:: |:       |  :   |:|  :   :|
Db     278 SL-----GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP 312


RESULT 6
Q91ZM6
ID   Q91ZM6      PRELIMINARY;      PRT;   433 AA.
AC   Q91ZM6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Tumor necrosis factor receptor type II (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RA   Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT   "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT   capillary endothelial cells and participate in TNF-alpha transport
RT   through the blood-brain barrier.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF420214; AAL16021.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     433    433
SQ   SEQUENCE   433 AA;  45723 MW;  75736D835E72CA4A CRC64;

  Query Match             21.0%;  Score 313.5;  DB 11;  Length 433;
  Best Local Similarity   35.1%;  Pred. No. 1.6e-19;
  Matches   59;  Conservative   29;  Mismatches   67;  Indels   13;  Gaps    4;

Qy      17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
           :: ||:|||| : :  | : | | |  |    :|| ||:|  |  |:  | : : |   |
Db      32 QMCCAKCPPGQYAKHFCNKTSDTVCADCAAGMFTQVWNHLHTCLSCSSSCSDDQVETHNC 91
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Qy      77 HATHNRACRCRTGFFA----HAG---FCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
           || | |    :     |:|    |:: : |.|| ||    | : |  |  | ||||
Db      92 TKKQNRVCACNADSYCALKLHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSACAPGTF 151

Qy     130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
           | ::||:: |:||| |: |     :||::| | :| | :  |  : ||
Db     152 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCASES--PTPSAVP 193


RESULT 7
Q98SM6
ID   Q98SM6      PRELIMINARY;      PRT;   651 AA.
AC   Q98SM6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Death receptor 6.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bridgham J.T., Johnson A.L.;
RT   "Expression of DR6 in the ovary.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF349908; AAK29666.2; -.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR003975; Shal_channel.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   PRINTS; PR01497; SHALCHANNEL.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   651 AA;  71003 MW;  BDC95A600DAB2C2A CRC64;

  Query Match             19.2%;  Score 287;  DB 13;  Length 651;
  Best Local Similarity   33.5%;  Pred. No. 5.2e-17;
  Matches   54;  Conservative   27;  Mismatches   80;  Indels    0;  Gaps    0;

Qy      11 DAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGERE 70
           |  | : |:| :|| ||:| : | : :   | |||   :|:  | :|||  |   |
Db      43 DRATNQELICDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCRKPCELPM 102

Qy      71 EEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFS 130
           |   | |  :| | :| |     |: :  || | ||   || ::: :|:||  ||||
Db     103 IEKTHCTALTDRECTCLSGTFQINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFS 162

Qy     131 ASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFP 171
           ||  :|: : :|    : :  ||:   | :| |    |
Db     163 DVPSSVMKCKTYTDCFGKNMVVVKPGTKESDNVCGSPASLP 203


RESULT 8
O57103
ID   O57103      PRELIMINARY;      PRT;   348 AA.
AC   O57103;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1979;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87847; AAB94364.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38184 MW;  34A5E668B27907B5 CRC64;

  Query Match             18.4%;  Score 275;  DB 12;  Length 348;
  Best Local Similarity   33.1%;  Pred. No. 3e-16;
  Matches   59;  Conservative   29;  Mismatches   82;  Indels    8;  Gaps    3;

Qy      10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
           :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db      33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy      69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
           : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db      93 NQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy     123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           || |||:| : ||:::|:|  : |   : : :     :|| ||  |   ||  :  :|
Db     152 PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTTGLSESISTSE 209


RESULT 9
O57108
ID   O57108      PRELIMINARY;      PRT;   348 AA.
AC   O57108;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1970;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88142; AAB94367.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38212 MW;  E555979057DEC91F CRC64;

  Query Match             18.4%;  Score 275;  DB 12;  Length 348;
  Best Local Similarity   33.1%;  Pred. No. 3e-16;
  Matches   59;  Conservative   29;  Mismatches   82;  Indels    8;  Gaps    3;

Qy      10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
           :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db      33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92
```

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Qy      69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
           : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db      93 NQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy     123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           || |||:| : ||:::|:|  : |   : : :     :|| ||  |   ||  :  :|
Db     152 PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTTGLSESISTSE 209


RESULT 10
O57277
ID   O57277      PRELIMINARY;      PRT;   348 AA.
AC   O57277;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog (J2R) (J2L).
GN   CRMB OR J2R OR J2L.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1996 /96-17, AND ZAIRE-1996 / 96-16;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-96-I-16;
RX   MEDLINE=21592287; PubMed=11734207;
RA   Shchelkunov S.N., Totmenin A.V., Babkin I.V., Safronov P.F.,
RA   Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
RA   Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B.,
RA   Sandakhchiev L.S.;
RT   "Human monkeypox and smallpox viruses: genomic comparison.";
RL   FEBS Lett. 509:66-70(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-96-I-16;
RA   Shchelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov V.V.,
RA   Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
RA   Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhchiev L.S.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88543; AAB94378.1; -.
DR   EMBL; U87841; AAB94358.1; -.
DR   EMBL; AF380138; AAL40648.1; -.
DR   EMBL; AF380138; AAL40460.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   348 AA;  38212 MW;  54019521556C2D8F CRC64;

  Query Match             18.4%;  Score 275;  DB 12;  Length 348;
  Best Local Similarity   33.1%;  Pred. No. 3e-16;
  Matches   59;  Conservative   29;  Mismatches   82;  Indels    8;  Gaps    3;

Qy      10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
           :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db      33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy      69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
           : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db      93 NQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy     123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
           || |||:| : ||:::|:|  : |   : : :     :|| ||  |   ||  :  :|
Db     152 PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTTGLSESISTSE 209


RESULT 11
O57100
ID   O57100      PRELIMINARY;      PRT;   349 AA.
AC   O57100;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NIGERIA-1971;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87844; AAB94361.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38239 MW;  DF6C280D478F2422 CRC64;

  Query Match             18.1%;  Score 270.5;  DB 12;  Length 349;
  Best Local Similarity   32.6%;  Pred. No. 7.4e-16;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels   13;  Gaps    5;

Qy      10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
           :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db      33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy      69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
           : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db      93 NQVETRSCNTTHNRICECSPGYYCLLKGASGCSTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy     123 PCPPGTFSASSSSSEQCQP---HRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGA 179
           || |||:| : ||:::|:|         : : :|:     :|| ||  |   ||  :  :
Db     152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209

Qy     180 E 180
           |
Db     210 E 210


RESULT 12
O57101
ID   O57101      PRELIMINARY;      PRT;   349 AA.
AC   O57101;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1977;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87845; AAB94362.1; -.
DR   HSSP; O14763; 1D0G.
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DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38311 MW;  02F65B00CFB858BE CRC64;

  Query Match             18.0%;  Score 268.5;  DB 12;  Length 349;
  Best Local Similarity   32.6%;  Pred. No. 1.1e-15;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels   13;  Gaps    5;

Qy      10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
           :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db      33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy      69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
           : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db      93 NQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy     123 PCPPGTFSASSSSSEQCQP---HRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGA 179
           || |||:| : ||:::|:|         : : :|:     :|| ||  |   ||  :  :
Db     152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209

Qy     180 E 180
           |
Db     210 E 210


RESULT 13
O57102
ID   O57102      PRELIMINARY;      PRT;   349 AA.
AC   O57102;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BENIN-1978;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87846; AAB94363.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38308 MW;  CBD2C949F994C59C CRC64;

  Query Match             18.0%;  Score 268.5;  DB 12;  Length 349;
  Best Local Similarity   32.6%;  Pred. No. 1.1e-15;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels   13;  Gaps    5;

Qy      10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
           :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db      33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy      69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
           : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db      93 NQVETRSCNTTHNRICECSPGYYCLLKGASGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy     123 PCPPGTFSASSSSSEQCQP---HRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGA 179
           || |||:| : ||:::|:|         : : :|:     :|| ||  |   ||  :  :
Db     152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209

Qy     180 E 180
           |
Db     210 E 210


RESULT 14
O57291
ID   O57291      PRELIMINARY;      PRT;   349 AA.
AC   O57291;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VARIOUS STRAINS;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88144; AAB94369.1; -.
DR   EMBL; U87842; AAB94359.1; -.
DR   EMBL; U87994; AAB94365.1; -.
DR   EMBL; U87995; AAB94366.1; -.
DR   EMBL; U88143; AAB94368.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   349 AA;  38295 MW;  CBD2C949ED2B8E7C CRC64;

  Query Match             18.0%;  Score 268.5;  DB 12;  Length 349;
  Best Local Similarity   32.6%;  Pred. No. 1.1e-15;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels   13;  Gaps    5;

Qy      10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
           :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db      33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy      69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
           : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db      93 NQVETRSCNTTHNRICECSPGYYCLLKGASGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy     123 PCPPGTFSASSSSSEQCQP---HRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGA 179
           || |||:| : ||:::|:|         : : :|:     :|| ||  |   ||  :  :
Db     152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209

Qy     180 E 180
           |
Db     210 E 210


RESULT 15
O57099
ID   O57099      PRELIMINARY;      PRT;   349 AA.
AC   O57099;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RC   STRAIN=SIERRA LEONE-1970;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87843; AAB94360.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38321 MW;  FE449028CC933F57 CRC64;

  Query Match             17.9%;  Score 267.5;  DB 12;  Length 349;
  Best Local Similarity   32.6%;  Pred. No. 1.4e-15;
  Matches   59;  Conservative   28;  Mismatches   81;  Indels   13;  Gaps    5;

Qy      10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
           :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db      33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy      69 REEEARACHATHNRACRCRTGFFA------HAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
             : | |:|: |||| | |  |::          |:    |  | || :  | : :  |
Db      93 NQVETRSCNTTHNRICECSPGYYCLLKGALGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy     123 PCPPGTFSASSSSSEQCQP---HRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGA 179
           || |||:| : ||:::|:|         : : :|:     :|| ||  |   ||  :  :
Db     152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTGLSESISTS 209

Qy     180 E 180
           |
Db     210 E 210


Search completed: January  6, 2003, 11:20:08
Job time : 75 secs
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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2003, 11:21:05 ; Search time 1970 Seconds
(without alignments)
2227.907 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09936024/runat_06012003_111607_12141/app_query.fasta_1.455
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09936024_@CGN_1_1_1349_@runat_06012003_111607_12141 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1183	79.3	1118	13	BI821789	BI821789 603035863
2	1147	76.9	863	14	BQ687526	BQ687526 AGENCOURT
3	1069	71.7	617	12	BE878908	BE878908 601492609
4	1064	71.4	572	14	BM767535	BM767535 K-EST0050
5	1060	71.1	1037	12	BG679499	BG679499 602627514
6	1055	70.8	1203	13	BM480312	BM480312 AGENCOURT
c 7	1034.5	69.4	728	14	BM680786	BM680786 UI-E-EO1-
8	1020	68.4	679	12	BE878006	BE878006 601489784
9	941.5	63.1	874	12	BF339551	BF339551 602039016
10	866	58.1	554	10	AW464298	AW464298 BP230015A
c 11	865.5	58.0	692	10	AW083241	AW083241 xc07a04.x
12	836	56.1	588	13	BI838357	BI838357 603083306
c 13	813	54.5	600	10	AW262121	AW262121 xq31d04.x
14	793	53.2	605	14	BM767088	BM767088 K-EST0049
15	793	53.2	605	14	BM767418	BM767418 K-EST0049
16	793	53.2	606	14	BM767446	BM767446 K-EST0049
c 17	788	52.9	568	14	BQ019285	BQ019285 UI-H-DT1-
18	781	52.4	596	14	BM767064	BM767064 K-EST0049
19	781	52.4	616	14	BM743072	BM743072 K-EST0016
20	769	51.6	486	14	BM831338	BM831338 K-EST0105
21	769	51.6	588	14	BM756087	BM756087 K-EST0034
22	769	51.6	593	14	BM759026	BM759026 K-EST0038
23	725	48.6	551	12	BE879166	BE879166 601486906
24	725	48.6	697	12	BE873766	BE873766 601483915
25	679	45.5	1216	14	BQ716334	BQ716334 AGENCOURT
26	676	45.3	384	14	BM738195	BM738195 K-EST0002
c 27	670	44.9	540	10	AW471440	AW471440 xw59e06.x
c 28	653	43.8	514	10	AW662363	AW662363 hi25f01.x
c 29	644	43.2	475	9	AI718743	AI718743 as95h04.x
30	633	42.5	524	14	BM833454	BM833454 K-EST0108
c 31	604	40.5	478	12	BF001490	BF001490 7g88h10.x
32	586	39.3	500	14	BM833463	BM833463 K-EST0108
c 33	584	39.2	515	10	AW083914	AW083914 xc25g02.x
c 34	580	38.9	459	10	AW014771	AW014771 UI-H-BI0-
c 35	566	38.0	448	14	BM672727	BM672727 UI-E-CQ0-
c 36	546	36.6	445	9	AI857725	AI857725 wl21a08.x
c 37	523	35.1	453	10	AW204999	AW204999 UI-H-BI1-
c 38	508	34.1	436	9	AI290210	AI290210 ql79g12.x
c 39	503	33.7	467	9	AA025673	AA025673 ze90h09.s
c 40	495	33.2	430	9	AI561219	AI561219 tq27c11.x
c 41	495	33.2	452	10	AW771720	AW771720 hl71a02.x
42	489	32.8	295	10	AW801019	AW801019 MR3-UM006
43	487.5	32.7	428	9	AA155701	AA155701 zo70e05.r
c 44	469	31.5	417	10	AW006931	AW006931 wt08b06.x
c 45	462	31.0	399	10	AW080544	AW080544 xc33a03.x

ALIGNMENTS

RESULT 1
BI821789
LOCUS BI821789 1118 bp mRNA linear EST 04-OCT-2001
DEFINITION 603035863F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176910 5', mRNA sequence.
ACCESSION BI821789
VERSION BI821789.1 GI:15933339
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1118)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11440  row: n  column: 15
            High quality sequence stop: 758.
FEATURES             Location/Qualifiers
     source          1. .1118
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5176910"
                     /clone_lib="NIH_MGC_115"
                     /lab_host="DH10B"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
BASE COUNT      223 a    377 c    339 g    179 t
ORIGIN

Alignment Scores:
Pred. No.:              9.73e-90        Length:         1118
Score:                  1183.00         Matches:        231
Percent Similarity:     98.30%          Conservative:   0
Best Local Similarity:  98.30%          Mismatches:     3
Query Match:            79.34%          Indels:         4
DB:                     13              Gaps:           0

US-09-936-024-1 (1-271) x BI821789 (1-1118)

Qy     38 ProThrThrCysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGlu 57
          ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db      3 CCCACGACGTGTGG-CCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAG 61

Qy     58 -ArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHi 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 GCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCA 121

Qy     77 sAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCy 97
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 CGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTG 181

Qy     97 sLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGl 117
          |||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db    182 CTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGAT-GCCCCGGGCACCCCCAGCCA 240

Qy    117 nAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGl 137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGA 300

Qy    137 uGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySe 157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTC 360

Qy    157 rSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValPr 177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db    361 TTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGTA-CC 419

Qy    177 oGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIl 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 AGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT 479

Qy    197 eLysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrPr 217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 CAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACC 539

Qy    217 oArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGl 237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 AAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGG 599

Qy    237 yAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetPr 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCC 659

Qy    257 oGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271
          ||||||||||||||||||||||||||||||||||||||||||
Db    660 CGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 702

RESULT 2
BQ687526
LOCUS       BQ687526                 863 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8345883 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250691
            5', mRNA sequence.
ACCESSION   BQ687526
VERSION     BQ687526.1  GI:21812842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2394  row: c  column: 12
            High quality sequence stop: 599.
FEATURES             Location/Qualifiers
     source          1. .863
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6250691"
                     /clone_lib="NIH_MGC_110"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of  California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      133 a    312 c    276 g    141 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              7.56e-87        Length:         863
Score:                  1147.00         Matches:        220
Percent Similarity:     94.87%          Conservative:   2
Best Local Similarity:  94.02%          Mismatches:     5
Query Match:            76.93%          Indels:         7
DB:                     14              Gaps:           2

US-09-936-024-1 (1-271) x BQ687526 (1-863)
```

```
Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGT 208

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 268

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     269 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 328

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 388

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 AACCGCGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 448

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     449 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 508

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     509 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGTTCCAGCTCAGAGCAGTGCCAG 568

Qy     141 ProHisArgAsnCysThr-AlaLeuGlyLeu-AlaLeuAsnValProGlySerSerSerH 160
           |||||||||||||||||| |||||||||||| |||||||||||||||||||||||||||||
Db     569 CCCCACCGCAACTGCACGNGCCCTGGGCCTGGGCCCTCAATGTGCCAGGCTCTTCCTCCC 628

Qy     160 isAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGly-Ala 179
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     629 ATGACACGCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAAGCT 688

Qy     180 GluGlu-CysGluArgAlaValIleAsp-PheValAlaPheGlnAspIleSerIleLysA 199
           ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||:
Db     689 GAGGAAGTGTGAGCGTGCCGTCATCGACTTTTGTGGCTTTCCAGGACATCTCCATCAAGA 748

Qy     199 rgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGly---ProThrProA 218
           ::|||||||||||||||||||||||||||||||||||||||||||   |||       ||||
Db     749 AGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAAGGGCTGGGGGTCCGAAACCCAA 808

Qy     218 rgAlaGly---ArgAlaAlaLeuGlnLeuLys 227
           ||||||||         ||||||||||:::
Db     809 GGGCGGGGCCGCCCCGGGCCTTGCAACTTGAA 840
```

RESULT 3
BE878908

LOCUS	BE878908 617 bp mRNA linear EST 20-OCT-2000
DEFINITION	601492609F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894794 5', mRNA sequence.
ACCESSION	BE878908
VERSION	BE878908.1 GI:10327684
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 617)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
	Plate: LLAM9685 row: a column: 03 High quality sequence stop: 617.
FEATURES	Location/Qualifiers
source	1. .617 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3894794" /clone_lib="NIH_MGC_69" /tissue_type="large cell carcinoma, undifferentiated" /lab_host="DH10B (phage-resistant)" /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."
BASE COUNT	91 a 224 c 203 g 99 t
ORIGIN	

Alignment Scores:

Pred. No.:	1.85e-80	Length:	617
Score:	1069.00	Matches:	202
Percent Similarity:	98.54%	Conservative:	0
Best Local Similarity:	98.54%	Mismatches:	3
Query Match:	71.70%	Indels:	1
DB:	12	Gaps:	0

US-09-936-024-1 (1-271) x BE878908 (1-617)

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Qy      53 TrpAsnTyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluGlu 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 TGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAG 63

Qy      73 AlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAla 92
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 GCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCG 123

Qy      93 HisAlaGlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaPro 112
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCG 183

Qy     113 GlyThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSer 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 GGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGC 243

Qy     133 SerSerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeu 152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 AGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTC 303

Qy     153 AsnValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeu 172
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 AATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTC 363

Qy     173 SerThrArgValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPhe 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 AGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTC 423

Qy     193 GlnAspIleSerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGly 212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 CAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGC 483

Qy     213 TrpGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeu 232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 TGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTC 543

Qy     233 ThrGluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArg 252
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 ACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGTG-CTGCAGGCGCTGCGC 602

Qy     253 ValAlaArgMetPro 257
           ||||||    |||
Db     603 GTGGCAGGATGCCCG 617
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RESULT 4
BM767535

```
LOCUS       BM767535                572 bp    mRNA    linear   EST 04-MAR-2002
DEFINITION  K-EST0050015 S1SNU5s2 Homo sapiens cDNA clone S1SNU5s2-3-E03 5',
            mRNA sequence.
ACCESSION   BM767535
VERSION     BM767535.1  GI:19097150
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 3  row: E  column: 03
            High quality sequence stop: 572.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S1SNU5s2-3-E03"
                     /clone_lib="S1SNU5s2"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Lymphoblast-like"
                     /cell_line="SNU-5"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library. After analyzing and
                     sequencing about 2,000 ~ 3,000 colonies in original cDNA
                     library, the abundant cDNAs were selected and amplified by
                     PCR reaction using vector region primer including T7
                     promotor as 5' primer and N(dT)14 as 3' primer. The PCR
                     products were used as template for synthesis of
                     biotinylated single stranded RNA by in vitro transcription
                     reaction. The synthesized RNA probes were hybridized with
                     antisense single stranded cDNAs prepared from original
                     liberary and incubated with avidin-gel. After removing
                     DNA-RNA hybrids by centrifuge, the subtracted cDNA
                     libraries were constructed by transformaion of the
                     remaining DNA into competent cells E. coli Top10F' with
                     electroporation method."
BASE COUNT       90 a    213 c    174 g     95 t
ORIGIN

Alignment Scores:
Pred. No.:              4.43e-80        Length:         572
Score:                  1064.00         Matches:        190
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0

Query Match:            71.36%          Indels:         0
DB:                     14              Gaps:           0

US-09-936-024-1 (1-271) x BM767535 (1-572)

Qy      40 ThrCysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCys 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 ACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGC 61

Qy      60 ArgTyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThr 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 CGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACC 121

Qy      80 HisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlu 99
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 CACAACCGCGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAG 181

Qy     100 HisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThr 119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 CACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACG 241

Qy     120 GlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCys 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 CAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGTTCCAGCTCAGAGCAGTGC 301

Qy     140 GlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSer 159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 CAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCC 361

Qy     160 HisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAla 179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 CATGACACGCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCT 421

Qy     180 GluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArg 199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     422 GAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGG 481

Qy     200 LeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAla 219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     482 CTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCG 541

Qy     220 GlyArgAlaAlaLeuGlnLeuLysLeuArg 229
           |||||||||||||||||||||||||||||
Db     542 GGCCGCGCGGCCTTGCAGCTGAAGCTGCGT 571

RESULT 5
BG679499
LOCUS       BG679499                1037 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602627514F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752507 5',
            mRNA sequence.
ACCESSION   BG679499
VERSION     BG679499.1  GI:13910896
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1037)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10610  row: k  column: 04
            High quality sequence stop: 762.
FEATURES             Location/Qualifiers
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     source          1. .1037
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4752507"
                     /clone_lib="NCI_CGAP_Skn4"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library  constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      153 a    364 c    337 g    183 t
ORIGIN

Alignment Scores:
Pred. No.:              2.06e-79        Length:         1037
Score:                  1060.00         Matches:        216
Percent Similarity:     86.77%          Conservative:   7
Best Local Similarity:  84.05%          Mismatches:     24
Query Match:            71.09%          Indels:         12
DB:                     12              Gaps:           3

US-09-936-024-1 (1-271) x BG679499 (1-1037)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     195 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 254

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     255 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 314

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     315 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTAGAGCGCTGCCGC 374

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     375 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 434

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db     435 AACCGTGCCTGCCGCTGCGC-ACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 493

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     494 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 553

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     554 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 613

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||||||||||   ||||||||||||||||||||||||||||||||||   |||
Db     614 CCCCACCGCAACTGCCG-GCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTTCCAT 672

Qy     161 AspThrLeu-CysThrSerCysThr-GlyPheProLeuSerThrArgValProGlyAlaG 180
           ||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     673 GACACCCTGTTGCACCAGCTGCACTTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTG 732

Qy     180 luGluCysGlu-ArgAlaVal-IleAspPheValAlaPhe------GlnAspIleSerIl 197
           |||||||||| |||||||| ||||||||||||   |||      :::   :::
Db     733 AGGAGTGTGAAGCGTGCCGTCCATCGACTTTGTGGGCTTTCCCAGGGAACATCTTCCATC 792

Qy     197 eLysArg-LeuGlnArgLeuLeuGlnAla---LeuGluAlaProGluGlyTrpGly-Pro 215
           :::||| ||||||   ::::::           |||   ||||||||||||||| |||
Db     793 AAGAAGGCTTGCAGGGGGTTGTGGCAGGCCCTTCCGAAGGCCCCGAGGGCTGGGGTTCCG 852

Qy     216 ThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeu 235
           ||||||||||||||                 ||||||||||:::
Db     853 ACACCAAGGGCGGGCGCCCGGCCTGCAGCTTGAAGCTTGCGTCGGCGGGTCCACGGGAGC 912

Qy     236 LeuGlyAla---GlnAspGlyAlaLeuLeuValArgLeu 247
```

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           |||      |||:::||||||||||||||||||||||
Db     913 TCCGGGGGGCCGCAAGAAGGGGCGCTGCTGGTGCGCCTG 951

RESULT 6
BM480312
LOCUS       BM480312                1203 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6424187 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491790
            5', mRNA sequence.
ACCESSION   BM480312
VERSION     BM480312.1  GI:18529354
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12112  row: n  column: 15
            High quality sequence start: 4
            High quality sequence stop: 560.
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5491790"
                     /clone_lib="NIH_MGC_67"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      202 a    452 c    311 g    238 t
ORIGIN

Alignment Scores:
Pred. No.:              6.58e-79        Length:         1203
Score:                  1055.00         Matches:        205
Percent Similarity:     78.65%          Conservative:   5
Best Local Similarity:  76.78%          Mismatches:     23
Query Match:            70.76%          Indels:         35
DB:                     13              Gaps:           5

US-09-936-024-1 (1-271) x BM480312 (1-1203)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 252

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     253 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 312

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     313 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 372

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     373 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 432

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    433 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 492

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120

Db    493 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 552

Qy    121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140

Db    553 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 612

Qy    141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160

Db    613 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 672

Qy    161 AspThrLeuCysThrSerCysThrGlyProProLeuSerThrArgValProGlyAla-Gl 180

Db    673 GACACCCTGTGCACCCGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAAGAGCCTGA 732

Qy    180 uGluCysGluArgAlaValIleAspPheVal---AlaPheGln---AspIleSerIleLy 198

Db    733 GGAGTGTGAGCGTGCCCCTCCATCCACTTTGTGGGCTTTTCCAGGACCTCTTCCTTCAAA 792

Qy    198 sArgLeuGlnArgLeuLeu---GlnAlaLeuGluAlaPro---------- 210

Db    793 AAGGTTGCAGCGGCTTGCTGGCAGGCCCCTCCAAGGCCCCGGGTAAGGCTTGGGTGTCCC 852

Qy    211 ----------GluGlyTrpGlyProThrProArg---------- 218

Db    853 AAACACCCTAGGGCGCGGACCGGGGAGTACCCCTAACCCTCATAACACTTACCCACCCCG 912

Qy    219 ----------AlaGlyArgAlaAlaLeuGlnLeuLy 227

Db    913 AATCACACCCACCTCCTTTGGCGCACCCAAATCCTCTGGCAGTTTCGCTTTGCACGCCCC 972

Qy    227 sLeuArgArgArgLeuThr 233

Db    973 TCTCTC-CGTCGCCTTACA 990
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```
RESULT 7
BM680786/c
LOCUS       BM680786                728 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  UI-E-EO1-ajc-j-12-0-UI.s1 UI-E-EO1 Homo sapiens cDNA clone
            UI-E-EO1-ajc-j-12-0-UI 3', mRNA sequence.
ACCESSION   BM680786
VERSION     BM680786.1  GI:18990682
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .728
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EO1-ajc-j-12-0-UI"
                     /clone_lib="UI-E-EO1"
                     /tissue_type="fetal eye"
                     /dev_stage="fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EO1 is a normalized cDNA library containing the
                     following tissue(s): fetal eye. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CGCGTATACC. This library was created for the program, Gene
                     Discovery in the Visual System, supported by National Eye
                     Institute (NEI).
                     TAG_LIB=UI-E-EO1
                     TAG_TISSUE=human fetal eye
                     TAG_SEQ=CGCGTATACC"
BASE COUNT      133 a    218 c    248 g    129 t
ORIGIN
```

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Alignment Scores:
Pred. No.:                1.85e-77      Length:          728
Score:                    1034.50       Matches:         196
Percent Similarity:       98.99%        Conservative:    0
Best Local Similarity:    98.99%        Mismatches:      1
Query Match:              69.38%        Indels:          1
DB:                       14            Gaps:            1

US-09-936-024-1 (1-271) x BM680786 (1-728)

Qy     75 AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAla 94

Db    704 GCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCT 645

Qy     95 GlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThr 114

Db    644 GGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACC 585

Qy    115 ProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSer 134

Db    584 CCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCC 525

Qy    135 SerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnVal 154

Db    524 AGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTG 465

Qy    155 ProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThr 174

Db    464 CCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACC 405

Qy    175 ArgValPro---GlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGln 193

Db    404 AGGGTACCAGCAGGAGCTGAGGAGTGTGAGCGTCCCGTCATCGACTTTGTGGCTTTCCAG 345

Qy    194 AspIleSerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrp 213

Db    344 GACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGG 285

Qy    214 GlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThr 233

Db    284 GGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACG 225

Qy    234 GluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgVal 253
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    224 GAGCTCCTGGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTG 165

Qy    254 AlaArgMetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    164 GCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 111

RESULT 8
BE878006
LOCUS       BE878006                679 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601489784F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891908 5',
            mRNA sequence.
ACCESSION   BE878006
VERSION     BE878006.1  GI:10326782
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9677  row: h  column: 21
            High quality sequence stop: 672.
FEATURES             Location/Qualifiers
     source          1. .679
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3891908"
                     /clone_lib="NIH_MGC_69"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      113 a    239 c    204 g    123 t
ORIGIN

Alignment Scores:
Pred. No.:              2.82e-76       Length:         679
Score:                  1020.00        Matches:        195
Percent Similarity:     99.49%         Conservative:   0
Best Local Similarity:  99.49%         Mismatches:     1
Query Match:            68.41%         Indels:         1
DB:                     12             Gaps:           0

US-09-936-024-1 (1-271) x BE878006 (1-679)

Qy     76 CysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGly 95
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGCCACGCCAC-CACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGT 59

Qy     96 PheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrPro 115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC 119

Qy    116 SerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSer 135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 AGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGC 179

Qy    136 SerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPro 155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    180 TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCA 239

Qy    156 GlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArg 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGG 299

Qy    176 ValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIle 195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 GTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATC 359

Qy    196 SerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyPro 215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 TCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCG 419

Qy    216 ThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeu 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 ACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTC 479

Qy    236 LeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArg 255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 CTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGG 539

Qy    256 MetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 ATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 587

RESULT 9
BF339551
LOCUS       BF339551                874 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  602039016F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186995
            5', mRNA sequence.
ACCESSION   BF339551
VERSION     BF339551.1  GI:11286006
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9508  row: p  column: 04
            High quality sequence stop: 701.
FEATURES             Location/Qualifiers
     source          1. .874
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4186995"
                     /clone_lib="NCI_CGAP_Brn64"
                     /tissue_type="glioblastoma with EGFR amplification"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      129 a    299 c    301 g    145 t
ORIGIN

Alignment Scores:
Pred. No.:              1.61e-69       Length:         874
Score:                  941.50         Matches:        181
Percent Similarity:     82.14%         Conservative:   3
Best Local Similarity:  80.80%         Mismatches:     27
```

```
Query Match:            63.15%      Indels:        14
DB:                     12          Gaps:          2

US-09-936-024-1 (1-271) x BF339551 (1-874)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 244

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 304

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     305 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 364

Qy      61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     365 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 424

Qy      81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 484

Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     485 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 544

Qy     121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
           ||||||     |||     |||||||||||||||||||||||||||||||||||||||||||
Db     545 TGCCAGCGTGCCCCCCAGGCAACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 604

Qy     141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
           ||||||   ||||||||||||   |||||||||||||||||||||||||||||||||||||
Db     605 CCCCACCG-AACTGCACGGCCTGGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 663

Qy     161 AspThrLeuCys-ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGl 180
           |||||||||    ||||||||||||||   |||   |||   :::       |||   ::
Db     664 GACACCCTGTGGCACCAGCTGCACTGGTTCCCCC---TCAGCACAGGGTACAGGAGTTGA 720

Qy     180 uGlu-CysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgL 200
           :||| ||||||||||||||                ||||||   :::||||||||||||
Db     721 TGAAGTGTGAGCGTGCCGTCTTCTGAGTTTGTGGCTTCCAGGGACTCTCCATCAAGAGGT 780

Qy     200 euGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaG 220
                                          |||       |||      |
Db     781 GC----------------------------GCGGTGTGGGCCTTAGGCCCGGAGGTGG 810

Qy     220 lyArgAla 222
           ||  |||
Db     811 GGTCCGCC 818

RESULT 10
AW464298
LOCUS       AW464298                554 bp    mRNA    linear   EST 24-FEB-2000
DEFINITION  BP230015A20G11 Soares normalized bovine placenta Bos taurus cDNA
            clone BP230015A20G11 5', mRNA sequence.
ACCESSION   AW464298
VERSION     AW464298.1  GI:7034466
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 554)
  AUTHORS   Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
            ,J.H.
  TITLE     Bovine ESTs
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Lewin, H. A.
            W. M. Keck Center for Comparative and Functional Genomics
            University of Illinois at Urbana-Champaign
            340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
            61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Funding for cattle EST sequencing was provided by the USDA National
            Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
            to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
            from Washington University Genome Center. Vector Trimmi g:
            Cross_match from Washington University Genome Center PHRAP suite.
            Sequences submitted are vector free and at least 200 bp in length.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Insert Length: 554   Std Error: 0.00
            Plate: BP230015A20  row: G  column: 11
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 554.
FEATURES             Location/Qualifiers
     source          1. .554
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone="BP230015A20G11"
                     /clone_lib="Soares normalized bovine placenta"
                     /sex="female"
                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI; The cDNA library was contributed by the
                     Soares laboratory and it  was constructed and normalized
                     as described by Bonaldo, M.F.,  Lennon, G. and Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. "
BASE COUNT       76 a    213 c    184 g     81 t
ORIGIN

Alignment Scores:
Pred. No.:              2.08e-63        Length:         554
Score:                  866.00          Matches:        147
Percent Similarity:     91.62%          Conservative:   6
Best Local Similarity:  88.02%          Mismatches:     14
Query Match:            58.08%          Indels:         0
DB:                     10              Gaps:           0

US-09-936-024-1 (1-271) x AW464298 (1-554)

Qy       2 AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAla 21
           |||      |||   |||||||||||||||||||||||||||||   |||||||||
Db      52 GCAAGCGCGCCCATCTACCCGTGGAGGGACGCAGAGACGGGGGAGTGGCTGGTGTGTGAC 111

Qy      22 GlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCys 41
           ||||||||||||||||||||||||||||||||||||   |||:::|||||||||||||||
Db     112 CAGTGCCCTCCGGGCACCTTTGTGCAGCGGCCTTGCGGCCGGAACAGCCCCACGACGTGC 171

Qy      42 GlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyr 61
           |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 GGTGCGTGCCCGCCGCGCCACTACACACAATTTTGGAACTACCTGGAGCGCTGCCGCTAC 231

Qy      62 CysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsn 81
           |||||||||:::|||||||||||||||||||||||||||||   |||   ||||||||||||
Db     232 TGCAACGTCATCTGCGGGGAGCGCGAGGAGGAGGCGCGGCCGTGCGGGGCCACCCACAAC 291

Qy      82 ArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAla 101
           ||||||||||||||||||:::|||||||||   ||||||||||||||||||||||||||||
Db     292 CGCGCCTGCCGCTGTCGGTCCGGTTTCTTCGAGCACGCCGGCTTCTGCCTGGAGCACGCG 351

Qy     102 SerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCys 121
           ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     352 TCCTGCCCGCCCGGCGCCGGCGTGGCTGCTCCCGGCACCCCCAGCCAGAACACACAGTGC 411

Qy     122 GlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnPro 141
           ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db     412 CAGCCGTGCCCCCCGGGCACCTTCTCCGCCAGCAGCTCGAGCTCGGAGCGGTGCCAGCCC 471
```

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Qy    142 HisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAsp 161
          ||||||||||||||||||||||||||||:::|||||||||||||||||      ||||||
Db    472 CACCGCAACTGCACAGCCCTGGGCCTGGCCGTCAATGTGCCTGGCTCCCCGTTACACGAC 531

Qy    162 ThrLeuCysThrSerCysThr 168
             |||||||||:::||||||
Db    532 GCCCTGTGCACCAACTGCACG 552

RESULT 11
AW083241/c
LOCUS       AW083241                692 bp    mRNA    linear   EST 14-OCT-1999
DEFINITION  xc07a04.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583534 3'
            similar to TR:O95407 O95407 DECOY RECEPTOR 3. ;contains L1.b1 MER22
            repetitive element ;, mRNA sequence.
ACCESSION   AW083241
VERSION     AW083241.1  GI:6038393
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 414.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2583534"
                     /clone_lib="NCI_CGAP_Co21"
                     /tissue_type="moderately differentiated adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Normalized to Cot >500.   Average insert size 1.04kb.
                     Normalized version of NCI_CGAP_Co18.   Library constructed
                     by Life Technologies."
BASE COUNT      136 a    205 c    235 g    115 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              3.05e-63        Length:         692
Score:                  865.50          Matches:        177
Percent Similarity:     89.95%          Conservative:   2
Best Local Similarity:  88.94%          Mismatches:     18
Query Match:            58.05%          Indels:         3
DB:                     10              Gaps:           1

US-09-936-024-1 (1-271) x AW083241 (1-692)

Qy     74 ArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHis 93
          |||:::                    |||     |||     |||||||||
Db    689 CGGTCCGCACGGCTTCCACGCACCACAACGTGCTGCCATCGCGCACGGTTTTTTGCGACG 630

Qy     94 AlaGlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGly 113
             |||   ||||||||||||||||||||||   ||||||||||||||||||||
Db    629 CTG---TTTCTGCTGGAGCACGCATCGTGTCCACCTGT-GCCGGCGTGATTGCCCCGGGC 574

Qy    114 ThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSer 133
          ||||||   |||||||||||||||||||||||||   ||||||||||||||:::|||
Db    573 ACCCCAGTCCAGAACACGCAGTGCCAGCCGTGCCCCCNAGGCACCTTCTCAGCAGCAAGC 514

Qy    134 SerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsn 153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT 454

Qy    154 ValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSer 173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 GTGCCAGGCTCTTCTTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGC 394

Qy    174 ThrArgValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGln 193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393 ACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAG 334

Qy    194 AspIleSerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrp 213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    333 GACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGG 274

Qy    214 GlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLys-LeuArgArgArgLeuTh 233
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    273 GGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAACTTGCGTCGGCGGCTCAC 214

Qy    233 rGluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgVa 253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    213 GGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGT 154

Qy    253 lAlaArgMetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    153 GGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 99

RESULT 12
BI838357
LOCUS       BI838357                588 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603083306F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222545 5',
            mRNA sequence.
ACCESSION   BI838357
VERSION     BI838357.1  GI:15949907
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11559  row: 1  column: 02
            High quality sequence stop: 588.
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5222545"
                     /clone_lib="NIH_MGC_120"
                     /lab_host="DH10B"
                     /note="Organ: pooled pancreas and spleen; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of spleen and pancreas from 28 yo
                     male.  Library is oligo-dT primed and directionally cloned
                     (EcoRV  site is destroyed upon cloning).  Average insert
                     size 1.5 kb, insert size range 1-2.5 kb.  Library is
                     normalized and enriched for  full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
```

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                tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT       97 a    224 c    171 g     95 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                7.6e-61        Length:          588
Score:                    836.00         Matches:         145
Percent Similarity:       97.97%         Conservative:    0
Best Local Similarity:    97.97%         Mismatches:      3
Query Match:              56.07%         Indels:          0
DB:                       13             Gaps:            0

US-09-936-024-1 (1-271) x BI838357 (1-588)

Qy      34 ArgArgAspSerProThrThrCysGlyProCysProProArgHisTyrThrGlnPheTrp 53
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGG 60

Qy      54 AsnTyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluGluAla 73
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCA 120

Qy      74 ArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHis 93
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CGGGCTTGCCACGCCACCCACAACCGCGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCAC 180

Qy      94 AlaGlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGly 113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGC 240

Qy     114 ThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSer 133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGT 300

Qy     134 SerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsn 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT 360

Qy     154 ValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSer 173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTGCCAGGCTCTTCCTCCCATGACACGCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGC 420

Qy     174 ThrArgValProGlyAlaGluGlu 181
           |||   |||||||||      |||
Db     421 ACCANGGTACCAGGTGAGCCAGAG 444

RESULT 13
AW262121/c
LOCUS       AW262121                600 bp    mRNA    linear   EST 28-DEC-1999
DEFINITION  xq31d04.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752231 3'
            similar to TR:O95407 O95407 DECOY RECEPTOR 3. ;contains TAR1.b1
            TAR1 repetitive element ;, mRNA sequence.
ACCESSION   AW262121
VERSION     AW262121.1  GI:6638937
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Possible reversed clone: polyT not found
            Seq primer: -40UP from Gibco
            High quality sequence stop: 410.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2752231"
                     /clone_lib="NCI_CGAP_Lu28"
                     /tissue_type="two pooled squamous cell carcinomas"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies."
BASE COUNT      120 a    177 c    199 g    102 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:                6.77e-59       Length:          600
Score:                    813.00         Matches:         156
Percent Similarity:       98.12%         Conservative:    1
Best Local Similarity:    97.50%         Mismatches:      3
Query Match:              54.53%         Indels:          0
DB:                       10             Gaps:            0

US-09-936-024-1 (1-271) x AW262121 (1-600)

Qy     112 ProGlyThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAla 131
           ||||||   |||:::|||||||||||||||||||||||||||||||||||||||||||||
Db     600 CCCGGGCACCCAGCCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCC 541

Qy     132 SerSerSerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAla 151
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Db     540 AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCNTGGGCNTGGCC 481

Qy     152 LeuAsnValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPhePro 171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 CTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC 421

Qy     172 LeuSerThrArgValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAla 191
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Qy     192 PheGlnAspIleSerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGlu 211
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Qy     212 GlyTrpGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArg 231
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Db     300 GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGG 241

Qy     232 LeuThrGluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeu 251
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Qy     252 ArgValAlaArgMetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271
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RESULT 14
BM767088
LOCUS       BM767088                605 bp    mRNA    linear   EST 04-MAR-2002
DEFINITION  K-EST0049137 S1SNU5s2 Homo sapiens cDNA clone S1SNU5s2-4-D01 5',
            mRNA sequence.
ACCESSION   BM767088
VERSION     BM767088.1  GI:19096703
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 605)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 4  row: D  column: 01
            High quality sequence stop: 605.
FEATURES             Location/Qualifiers
     source          1. .605
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                     /cell_line="SNU-5"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library. After analyzing and
                     sequencing about 2,000 ~ 3,000 colonies in original cDNA
                     library, the abundant cDNAs were selected and amplified by
                     PCR reaction using vector region primer including T7
                     promotor as 5' primer and N(dT)14 as 3' primer. The PCR
                     products were used as template for synthesis of
                     biotinylated single stranded RNA by in vitro transcription
                     reaction. The synthesized RNA probes were hybridized with
                     antisense single stranded cDNAs prepared from original
                     liberary and incubated with avidin-gel. After removing
                     DNA-RNA hybrids by centrifuge, the subtracted cDNA
                     libraries were constructed by transformaion of the
                     remaining DNA into competent cells E. coli Top10F' with
                     electroporation method."
BASE COUNT       87 a    221 c    203 g     94 t
ORIGIN

Alignment Scores:
Pred. No.:                3.32e-57        Length:         605
Score:                    793.00          Matches:        135
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              53.19%          Indels:         0
DB:                       14              Gaps:           0

US-09-936-024-1 (1-271) x BM767088 (1-605)

Qy       1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
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Db     201 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGT 260

Qy      21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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Db     261 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 320

Qy      41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Qy     101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db     501 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAG 560

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RESULT 15
BM767418
LOCUS       BM767418                605 bp    mRNA    linear   EST 04-MAR-2002
DEFINITION  K-EST0049884 S1SNU5s2 Homo sapiens cDNA clone S1SNU5s2-5-B04 5',
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ACCESSION   BM767418
VERSION     BM767418.1  GI:19097033
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 605)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 5  row: B  column: 04
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                     /cell_type="Lymphoblast-like"
                     /cell_line="SNU-5"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
```

obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformaion of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

BASE COUNT 87 a 221 c 203 g 94 t
ORIGIN

Alignment Scores:

Pred. No.:	3.32e-57	Length:	605
Score:	793.00	Matches:	135
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	53.19%	Indels:	0
DB:	14	Gaps:	0

US-09-936-024-1 (1-271) x BM767418 (1-605)

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Qy      1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGT 260

Qy     21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG 320

Qy     41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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Db    381 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCAC 440

Qy     81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Db    441 AACCGCGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 500

Qy    101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Search completed: January 6, 2003, 12:04:15
Job time : 1972 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:33 ; Search time 37 Seconds
(without alignments)
704.120 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	340.5	22.8	461	1	A35356	tumor necrosis fac
2	333.5	22.4	459	2	I48854	gene murine tumour
3	332.5	22.3	474	2	B38634	tumor necrosis fac
4	299.5	20.1	435	2	I54182	tumor necrosis fac
5	289	19.4	651	2	JC7705	death receptor-6 -
6	260	17.4	348	2	T28623	hypothetical prote
7	260	17.4	349	2	D72175	G2R protein - vari
8	260	17.4	349	2	D36858	gene G4R protein -
9	234.5	15.7	325	2	B43692	T2 protein - rabbi
10	215.5	14.5	277	2	I37552	OX40 homolog - hum
11	211.5	14.2	271	2	S12783	OX40 antigen precu
12	211	14.2	277	2	A60771	B-cell activation
13	210.5	14.1	326	1	GQVZML	T2 protein - myxom
14	203	13.6	305	2	A46476	B cell-associated
15	194.5	13.0	272	2	I48700	gene ox40 protein
16	185	12.4	256	2	B32393	T-cell antigen 4-1
17	182	12.2	595	2	A42086	CD30 antigen precu
18	174	11.7	255	2	I38426	lymphocyte activat
19	171.5	11.5	416	1	JN0006	nerve growth facto
20	168	11.3	425	1	A26431	nerve growth facto
21	158	10.6	427	1	GQHUN	nerve growth facto
22	155.5	10.4	327	2	A46484	apoptosis-mediatin
23	148.5	10.0	1574	2	T13954	MEGF6 protein - ra
24	148	9.9	250	1	A49053	CD27 antigen precu
25	147.5	9.9	5376	2	T42215	zonadhesin - mouse
26	146.5	9.8	260	1	A46517	CD27 antigen precu
27	145	9.7	335	2	A40036	apoptosis-mediatin
28	143	9.6	1620	2	T27283	hypothetical prote
29	140	9.4	314	2	I37383	FAS soluble protei
30	137.5	9.2	324	2	JC2395	Fas antigen precur
31	135.5	9.1	1299	2	T43251	furin (EC 3.4.21.7
32	135	9.1	2321	2	S78549	notch3 protein - h
33	130.5	8.8	454	1	GQMST1	tumor necrosis fac
34	128.5	8.6	3635	2	T10053	laminin alpha 5 ch
35	127	8.5	1192	2	S69000	laminin gamma 2 ch
36	125.5	8.4	1548	2	S34583	serine proteinase
37	124.5	8.4	1713	2	A55347	adhesive ligand ep
38	123.5	8.3	455	1	GQHUT1	tumor necrosis fac
39	123.5	8.3	493	2	JC5486	membrane glycoprot
40	122.5	8.2	2824	2	T22759	hypothetical prote
41	121	8.1	3106	1	S53868	laminin alpha-2 ch
42	120	8.0	1609	1	MMHUB2	laminin gamma-1 ch
43	119.5	8.0	3084	1	MMMSA	laminin alpha-1 ch
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ALIGNMENTS

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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
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A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A;Reference number: A36475; MUID:91045991; PMID:2172983
A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
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R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.;
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A;Reference number: A48416; MUID:91370690; PMID:1966549
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
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A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstrat
A;Reference number: A36007; MUID:90349572; PMID:2166946
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
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A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A;Reference number: A23666; MUID:91056048; PMID:2173696
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>

R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934; PMID:7821811
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Qy     103 CPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDT 162
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Db     143 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVA----IPGNASMDA 198

Qy     163 LCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE-----GWGPTP 217
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Qy     218 RA----GRAALQLKLRRRLTELLGAQDGALLVRLLQAL---RVARMP-GLERSVRERFLP 269
             |    |  || : |   :| |     | |:: ::  :   :| : |  |:|  :   ||
Db     250 PAEGSTGDFALPVGLIVGVTAL-----GLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLP 304
```

RESULT 2
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848; PMID:7873884
A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>

  Query Match 22.4%; Score 333.5; DB 2; Length 459;
  Best Local Similarity 29.7%; Pred. No. 6.3e-18;
  Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

```
Qy      17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
           :: ||:|||| :|:  | : | | |  |     ||| ||     |  |:  |   : | |||
Db      37 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRAC 96

Qy      77 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
             || | |  | :     |:|    |:  : | || || :   |: |  |: | ||||
Db      97 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 156

Qy     130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
           | ::||::  |:||| |: |     :||::| | :|     : :  | :  |   |
Db     157 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 212

Qy     186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 240
            :|    |:    :  :| :|       | ||       |  :| : |   :| |
Db     213 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 257

Qy     241 GALLVRLLQAL----RVARMPGLERSVRERFLP 269
           | |:: |:       |  :   |:|  :   :|
Db     258 GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP 290
```

RESULT 3
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>

  Query Match 22.3%; Score 332.5; DB 2; Length 474;
  Best Local Similarity 29.7%; Pred. No. 7.7e-18;
  Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

```
Qy      17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
           :: ||:|||| :|:  | : | | |  |    ||| ||    |  |:  |   : | |||
Db      52 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRAC 111

Qy      77 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
             || | |  | :     |:|    |:  : | || || :   |: |  |: | ||||
Db     112 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 171

Qy     130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
           | ::||:: |:||| |: |     :||::| | :|     : :  | :  |   |
Db     172 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 227

Qy     186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 240
           :|    |:    :   :| :|      | ||       |  :| : |   :| |
Db     228 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 272

Qy     241 GALLVRLLQAL----RVARMPGLERSVRERFLP 269
           | |:: |:  :    |  :   |:|  :   :|
Db     273 GLLMLGLVNCIILVQRKKKPSCLQRDAKVPHVP 305


RESULT 4
I54182
tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A;Reference number: I54182; MUID:93252381; PMID:8486360
A;Accession: I54182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

  Query Match             20.1%;  Score 299.5;  DB 2;  Length 435;
  Best Local Similarity   32.0%;  Pred. No. 2.2e-15;
  Matches   74;  Conservative   27;  Mismatches  101;  Indels   29;  Gaps    9;

Qy      13 ETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGER 69
           |   |: |::|||||:|   | |   | |  |   | : ||||   : || |: : |
Db      52 EPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG-- 109

Qy      70 EEEARACHATHNRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQ 122
             ||    | :     |||: | |  | : ||  |    : ||||    :       |  |
Db     110 LEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCV 168

Qy     123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEEC 182
           ||  | |  :|| | :|||| |    ||     ||::  || | :    ||   : |
Db     169 PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE-PLPPEMSGTMLM 227

Qy     183 ERAVIDFVAFQDIS------------IKRLQRLLQALEAPEGWGPTPRAG 220
           ::    |  ::              ::|  ||:   |:| || | ||
Db     228 LAVLLPLAFFLLLATVFSCIWKSHPSLCRKLGSLLK--RRPQGEGPNPVAG 276


RESULT 5
JC7705
death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TMM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

  Query Match             19.4%;  Score 289;  DB 2;  Length 651;
  Best Local Similarity   33.5%;  Pred. No. 2e-14;
  Matches   54;  Conservative   27;  Mismatches   80;  Indels    0;  Gaps    0;

Qy      11 DAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGERE 70
           |  | : |:| :|| ||:| : | : :   | |||   :|:  | :|||  |   |
Db      43 DRATNQELICDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCRKPCELPM 102

Qy      71 EEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFS 130
             |  | |  :| | | :| |     |: :  || | ||   || ::: :|:||  ||||
Db     103 IEKTHCTALTDRECTCLSGTFQINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFS 162

Qy     131 ASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFP 171
             ||  :|: : :|    : :  ||:   | :| |    |
Db     163 DVPSSVMKCKTYTDCFGKNMVVVKPGTKESDNVCXSPASLP 203


RESULT 6
T28623
hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin,
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus g
A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-348 <MAS>
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

  Query Match             17.4%;  Score 260;  DB 2;  Length 348;
  Best Local Similarity   32.2%;  Pred. No. 1.7e-12;
  Matches   59;  Conservative   26;  Mismatches   90;  Indels    8;  Gaps    3;

Qy       5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN 63
           |    :| |      | |  |||||:  | |   : | | ||    :|   |:|  |  ||
Db      27 PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 86

Qy      64 VLCGEREEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQ 117
             |  : | |:|: |||| | |  |::      :    |:    | | || :  |
Db      87 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 145

Qy     118 NTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
           :  | ||  ||:| : ||:::|:|  | |   : : :     :|| ||  |   ||  :
Db     146 DVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL 205

Qy     178 GAE 180
           :|
Db     206 TSE 208


RESULT 7
D72175
```

G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A;Reference number: A72150
A;Accession: D72175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A;Experimental source: strain Garcia-1966
C;Genetics:
A;Gene: G2R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 349;
Best Local Similarity 32.2%; Pred. No. 1.7e-12;
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

```
Qy       5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN 63
           |    :| |     | |  |||||:  | |   : | | ||    :|   |:|  |  ||
Db      28 PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 87

Qy      64 VLCGEREEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQ 117
             |   : | |:|: |||| | |  |::      :    |:    |  | || :  |
Db      88 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 146

Qy     118 NTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
           :  | ||  ||:| : ||:::|:|  | |   : : :     :|| ||  |   ||  :
Db     147 DVICSPCGFGTYSYTVSSTDKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL 206

Qy     178 GAE 180
           :|
Db     207 TSE 209
```

RESULT 8
D36858
gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <BLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol
submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A;Reference number: S46868
A;Accession: S46888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <KOL>
A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A;Experimental source: strain India-1967, isolate Ind3
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A;Reference number: S32385; MUID:93202281; PMID:8384129
A;Accession: S32385
A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Cross-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
C;Genetics:
A;Gene: G4R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;32-66/Domain: NGF receptor repeat homology <NGF>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 17.4%; Score 260; DB 2; Length 349;
Best Local Similarity 32.2%; Pred. No. 1.7e-12;
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

```
Qy       5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN 63
           |    :| |     | |  |||||:  | |   : | | ||    :|   |:|  |  ||
Db      28 PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 87

Qy      64 VLCGEREEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQ 117
             |   : | |:|: |||| | |  |::      :    |:    |  | || :  |
Db      88 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 146

Qy     118 NTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
           :  | ||  ||:| : ||:::|:|  | |   : : :     :|| ||  |   ||  :
Db     147 DVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL 206

Qy     178 GAE 180
           :|
Db     207 TSE 209
```

RESULT 9
B43692
T2 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: B43692
R;Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A;Reference number: A43692; MUID:87321103; PMID:2820128
A;Accession: B43692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-325 <UPT>
A;Cross-references: GB:M17433
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 15.7%; Score 234.5; DB 2; Length 325;
Best Local Similarity 32.9%; Pred. No. 1.4e-10;
Matches 52; Conservative 19; Mismatches 76; Indels 11; Gaps 3;

```
Qy      18 LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACH 77
           | || | || :  | |   | | | ||    :|   |:   |  |   |     |:: |
Db      38 LCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGHLSESQPCD 97

Qy      78 ATHNRACRCRTGFFA------HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA 131
             ||:| | | || :           |     || | || :  | : :| |: ||| |:|
Db      98 RTHDRVCNCSTGNYCLLKGQNGCRICAPQTKCPAGYGV-SGHTRAGDTLCEKCPPHTYSD 156

Qy     132 SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTG 169
           | | :|:|     |  ::|  |       ::| ||:  |
Db     157 SLSPTERCGTSFNYISVGFNL----YPVNETSCTTTAG 190
```

RESULT 10
I37552
OX40 homolog - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: I37552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fona
Eur. J. Immunol. 24, 677-683, 1994

```
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment c
A;Reference number: I37552; MUID:94170844; PMID:7510240
A;Accession: I37552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match            14.5%;  Score 215.5;  DB 2;  Length 277;
  Best Local Similarity   27.0%;  Pred. No. 3.2e-09;
  Matches   72;  Conservative   22;  Mismatches  104;  Indels   69;  Gaps   11;

Qy       6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN 63
           |||  |        | :| ||  :   | |   | | || |  |    :    : | :||
Db      35 TYPSNDR------CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCN 88

Qy      64 VLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQP 123
           :  |   |  : | || :  |||| |              |  ||                | |
Db      89 LRSG--SERKQLCTATQDTVCRCRAG-------TQPLDSYKPG------------VDCAP 127

Qy     124 CPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTS---CTGFPLSTRVPGAE 180
           |||| |  |   :: |:|  |||  |      | |:| | :|         |  |: | |
Db     128 CPPGHF--SPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPAR 185

Qy     181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGW-----GPTPR-----AGRAALQLKLRR 230
                                    ::  | |     ||: |      |||   :
Db     186 PI----------------------TVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLG 222

Qy     231 RLTELLGAQDGALLVRLLQALRVARMP 257
           :  |||    |:|: |    |  |:|
Db     223 LVLGLLGPL--AILLALYLLRRDQRLP 247


RESULT 11
S12783
OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A;Reference number: S12783; MUID:90214614; PMID:2157591
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domain: transmembrane #status predicted <TMM>

  Query Match            14.2%;  Score 211.5;  DB 2;  Length 271;
  Best Local Similarity   31.5%;  Pred. No. 6.4e-09;
  Matches   53;  Conservative   18;  Mismatches   54;  Indels   43;  Gaps    8;

Qy       6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN 63
           |||     :| :  | :| ||  :   |     | | || |  | :  ||   ::|  ||
Db      30 TYP-----SGHK-CCRECQPGHGMVSRCDHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCN 83

Qy      64 VLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGT-PSQNT--- 119
             |   |  : |  | :  |:||                          ||| | |::
Db      84 HRSG--SELKQNCTPTEDTVCQCR-----------------------PGTQPRQDSSHK 117

Qy     120 ---QCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
              | ||||| |  |  |:: |:|  |||  |  :  | |:| ||:|
Db     118 LGVDCVPCPPGHF--SPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163


RESULT 12
A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor a
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            14.2%;  Score 211;  DB 2;  Length 277;
  Best Local Similarity   30.5%;  Pred. No. 7.1e-09;
  Matches   46;  Conservative   21;  Mismatches   76;  Indels    8;  Gaps    3;

Qy      20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC 76
           |: | ||  :   |   : | | ||    :   ||    |   :||:   | | ::
Db      38 CSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTS 97

Qy      77 HATHNRACRCRTGFFAHA---GFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 133
              :  | |  |:   :      |: | || || ||    |  :| |:|| | ||  |
Db      98 ET--DTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVS 155

Qy     134 SSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
           |: |:| |  :|    | :   |::  | :|
Db     156 SAFEKCHPWTSCETKDLVVQQAGTNKTDVVC 186


RESULT 13
GQVZML
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis fa
A;Reference number: A40566; MUID:91335768; PMID:1651597
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            14.1%;  Score 210.5;  DB 1;  Length 326;
```

```
  Best Local Similarity   30.4%;  Pred. No. 9.1e-09;
  Matches   48;  Conservative   19;  Mismatches   80;  Indels   11;  Gaps    3;

Qy      18 LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACH 77
           | |  ||||::  | |    | | | ||    :|   |:  |  |   |     |:::|
Db      38 LCCTSCPPGSYASRLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSESQSCD 97

Qy      78 ATHNRACRCRTGFFA------HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA 131
             | :| | |  | :           |     || | || :  | : :  |  ||  |:|
Db      98 KTRDRVCDCSAGNYCLLKGQEGCRICAPKTKCPAGYGV-SGHTRTGDVLCTKCPRYTYSD 156

Qy     132 SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTG 169
           : ||:| |    |  ::   |       :|| ||:  |
Db     157 AVSSTETCTSSFNYISVEFNL----YPVNDTSCTTTAG 190


RESULT 14
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A;Reference number: A46476; MUID:92105763; PMID:1370315
A;Accession: A46476
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <TOR>
A;Cross-references: GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586; PMID:1281194
A;Accession: A46515
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-287,'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N
A;Experimental source: BALB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>

  Query Match             13.6%;  Score 203;  DB 2;  Length 305;
  Best Local Similarity   31.1%;  Pred. No. 3.1e-08;
  Matches   47;  Conservative   19;  Mismatches   77;  Indels    8;  Gaps    3;

Qy      20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC 76
           |  | ||: :   |     | | ||    ::  ||   ||   |:|    | | ::
Db      38 CDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGT- 96

Qy      77 HATHNRACRCRTGFFA---HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 133
             |  :  | |: |          | :|  | ||| ||:   | : :| | ||| | ||  |
Db      97 -AESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQS 155

Qy     134 SSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
           |  |:| |  :|    | :   |:|  : :|
Db     156 SLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC 186


RESULT 15
I48700
gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell in
A;Reference number: I48700; MUID:94044750; PMID:8228223
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A;Reference number: I48334; MUID:95255413; PMID:7737295
A;Accession: I48334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match             13.0%;  Score 194.5;  DB 2;  Length 272;
  Best Local Similarity   30.4%;  Pred. No. 1.2e-07;
  Matches   51;  Conservative   16;  Mismatches   58;  Indels   43;  Gaps    8;

Qy       6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN 63
           |||     :| :  | :| ||  :   |      | | ||    | :  ||   ::|  ||
Db      31 TYP-----SGHK-CCRECQPGHGMVSRCDHTRDTLCHPCETGFYNEAVNYDTCKQCTQCN 84

Qy      64 VLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGT-PSQNT--- 119
             |   |  : |  | :  ||||                              |||  | |::
Db      85 HRSG--SELKQNCTPTQDTVCRCR-----------------------PGTQPRQDSGYK 118

Qy     120 ---QCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
              | |||||  |  |  ::: |:|  |||  |     | | | | :|
Db     119 LGVDCVPCPPGHF--SPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164


Search completed: January  6, 2003, 11:21:00
Job time : 39 secs
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